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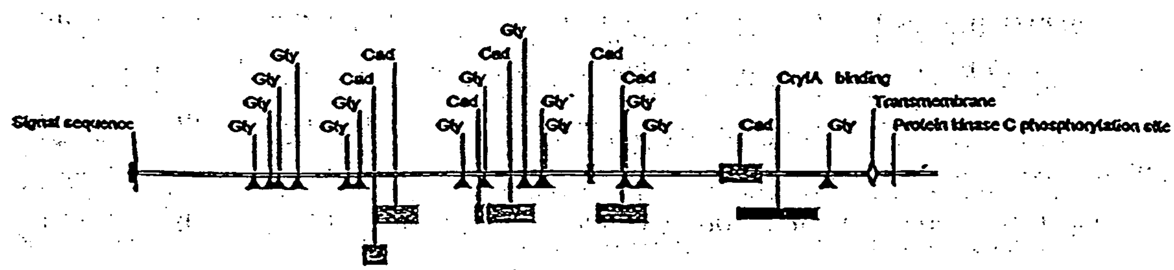
(54) Title: NOVEL *BT* TOXIN RECEPTORS FROM LEPIDOPTERAN INSECTS AND METHODS OF USE



(57) Abstract: The invention relates to *Bt* toxin resistance management. The invention particularly relates to the isolation and characterization of nucleic acid and polypeptides for a novel *Bt* toxin receptor. The nucleic acid and polypeptides are useful in identifying and designing novel *Bt* toxin receptor ligands including novel insecticidal toxins.

NOVEL *BT* TOXIN RECEPTORS FROM LEPIDOPTERAN INSECTS AND METHODS OF USE

FIELD OF THE INVENTION

The field of the invention is manipulating *Bt* toxin susceptibility in plant pests. The field of the invention relates to the isolation and characterization of nucleic acid and polypeptides for a novel *Bt* toxin receptor. The nucleic acid and polypeptides are useful in developing new insecticides.

BACKGROUND OF THE INVENTION

Traditionally, growers used chemical pesticides as a means to control agronomically important pests. The introduction of transgenic plants carrying the delta-endotoxin from *Bacillus thuringiensis* (*Bt*) afforded a non-chemical method of control. *Bt* toxins have traditionally been categorized by their specific toxicity towards specific insect categories. For example, the CryI group of toxins are toxic to Lepidoptera. The CryI group includes, but is not limited to, CryIA(a), CryIA(b) and CryIA(c). See Hofte *et al* (1989) *Microbiol Rev* 53: 242-255.

Lepidopteran insects cause considerable damage to maize crops throughout North America and the world. One of the leading pests is *Ostrinia nubilalis*, commonly called the European Corn Borer (ECB). Genes encoding the crystal proteins CryIA(b) and CryIA(c) from *Bt* have been introduced into maize as a means of ECB control. These transgenic maize hybrids have been effective in control of ECB. However, developed resistance to *Bt* toxins presents a challenge in pest control. See McGaughey *et al.* (1998) *Nature Biotechnology 16*: 144-146; Estruch *et al.* (1997) *Nature Biotechnology 15*:137-141; Roush *et al.* (1997) *Nature Biotechnology 15* 816-817; and Hofte *et al* (1989) *Microbiol Rev* 53: 242-255.

The primary site of action of Cry1 toxins is in the brush border membranes of the midgut epithelia of susceptible insect larvae such as lepidopteran insects. CryIA toxin binding polypeptides have been characterized from a variety of *Lepidopteran* species. A CryIA(c) binding polypeptide with homology to an aminopeptidase N has been reported from *Manduca sexta*, *Lymantria dispar*, *Helicoverpa zea* and *Heliothis virescens* . See Knight et al (1994) *Mol Micro 11*: 429-436; Lee *et al.* (1996) *Appl*

Environ Micro 63: 2845-2849; Gill *et al.* (1995) *J Biol. Chem 270*: 27277-27282; and Garczynski *et al.* (1991) *Appl Environ Microbiol 10*: 2816-2820.

Another *Bt* toxin binding polypeptide (BTR1) cloned from *M. sexta* has homology to the cadherin polypeptide superfamily and binds CryIA(a), CryIA(b) and CryIA(c). See Vadlamudi *et al.* (1995) *J Biol Chem 270(10)*:5490-4, Keeton *et al.* (1998) *Appl Environ Microbiol 64(6)*:2158-2165; Keeton *et al.* (1997) *Appl Environ Microbiol 63(9)*:3419-3425 and U.S. Patent Patent No: 5,693,491.

A subsequently cloned homologue to BTR1 demonstrated binding to CryIA(a) from *Bombyx mori* as described in Ihara *et al.* (1998) *Comparative Biochemistry and Physiology, Part B 120*:197-204 and Nagamatsu *et al.* (1998) *Biosci. Biotechnol. Biochem. 62(4)*:727-734.

Identification of the plant pest binding polypeptides for *Bt* toxins are useful for investigating *Bt* toxin-*Bt* toxin receptor interactions, selecting and designing improved toxins, developing novel insecticides, and new *Bt* toxin resistance management strategies.

SUMMARY OF THE INVENTION

Compositions and methods for modulating susceptibility of a cell to *Bt* toxins are provided. The compositions include *Bt* toxin receptor polypeptides, and fragments and variants thereof, from the lepidopteran insects European corn borer(ECB, *Ostrinia nubilalis*), corn earworm (CEW, *Heliothis Zea*), and fall armyworm (FAW, *Spodoptera frugiperda*). The polypeptides bind Cry1A toxins, more particularly Cry1A(b). Nucleic acids encoding the polypeptides, antibodies specific to the polypeptides, as well as nucleic acid constructs for expressing the polypeptides in cells of interest are also provided.

The methods are useful for investigating the structure-function relationships of *Bt* toxin receptors; investigating the toxin-receptor interactions; elucidating the mode of action of *Bt* toxins; screening and identifying novel *Bt* toxin receptor ligands including novel insecticidal toxins; and designing and developing novel *Bt* toxin receptor ligands.

The methods are useful for managing *Bt* toxin resistance in plant pests, and protecting plants against damage by plant pests.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 schematically depicts the location of the signal sequence, putative glycosilation sites, cadherin-like domains, transmembrane segment, CrylA binding region and protein kinase C phosphorylation site of the *Bt* toxin receptor from *Ostrinia nubilalis*; the nucleotide sequence of the receptor set forth in SEQ ID NO:1 and the corresponding deduced amino acid sequence in SEQ ID NO:2.

DETAILED DESCRIPTION OF THE INVENTION

The invention is directed to novel receptor polypeptides that bind *Bt* toxin, the receptor being derived from the order *lepidoptera.* The receptors of the invention include those receptor polypeptides that bind *Bt* toxin and are derived from the *lepidopteran* superfamily *Pyraloidea* and particularly from the species *Ostrinia*, specifically *Ostrinia nubilalis*; those derived from *Spodoptera frugiperda* (*S. frugiperda*); and those derived from *Heliothus Zea* (*H. Zea*). The polypeptides have homology to members of the cadherin superfamily of proteins.

Accordingly, compositions of the invention include isolated polypeptides that are involved in *Bt* toxin binding. In particular, the present invention provides for isolated nucleic acid molecules comprising nucleotide sequences encoding the amino acid sequences shown in SEQ ID NOs: 2, 4, and 6; or the nucleotide sequences having the DNA sequences deposited in a plasmid in a bacterial host as Patent Deposit No. PTA-278, PTA-1760, and PTA-2222. Further provided are polypeptides having an amino acid sequence encoded by a nucleic acid molecule described herein, for example those set forth in SEQ ID NOs: 1, 3, and 5; those deposited in a plasmid in a bacterial host as Patent Deposit Nos. PTA-278, PTA-1760, and PTA-2222; and fragments and variants thereof.

Plasmids containing the nucleotide sequences of the invention were deposited with the Patent Depository of the American Type Culture Collection (ATCC), Manassas, Virginia on June 25, 1999; April 25, 2000; and July 11, 2000; and assigned Patent Deposit Nos. PTA-278, PTA-1760, and PTA-2222. These deposits will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. These deposits

were made merely as a convenience for those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112.

The term "nucleic acid" refers to all forms of DNA such as cDNA or genomic DNA and RNA such as mRNA, as well as analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecules can be single stranded or double stranded. Strands can include the coding or non-coding strand.

The invention encompasses isolated or substantially purified nucleic acid or polypeptide compositions. An “isolated” or “purified” nucleic acid molecule or polypeptide, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an “isolated” nucleic acid is free of sequences (preferably polypeptide encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A polypeptide that is substantially free of cellular material includes preparations of polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating polypeptide. When the polypeptide of the invention or biologically active portion thereof is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-polypeptide-of-interest chemicals.

It is understood, however, that there are embodiments in which preparations that do not contain the substantially pure polypeptide may also be useful. Thus, less pure preparations can be useful where the contaminating material does not interfere with the specific desired use of the peptide. The compositions of the invention also encompass fragments and variants of the disclosed nucleotide sequences and the polypeptides encoded thereby.

The compositions of the invention are useful for, among other uses, expressing the receptor polypeptides in cells of interest to produce cellular or isolated preparations of the polpeptides for investigating the structure-function relationships of

Bt toxin receptors; investigating the toxin-receptor interactions; elucidating the mode of action of *Bt* toxins; screening and identifying novel *Bt* toxin receptor ligands including novel insecticidal toxins; and designing and developing novel *Bt* toxin receptor ligands including novel insecticidal toxins.

The isolated nucleotide sequences encoding the receptor polypeptides of the invention are expressed in a cell of interest; and the *Bt* toxin receptor polypeptides produced by the expression is utilized in intact cell or *in-vitro* receptor binding assays, and/or intact cell toxicity assays. Methods and conditions for *Bt* toxin binding and toxicity assays are known in the art and include but are not limited to those described in United States Patent NO: 5,693,491; T.P. Keeton *et al.* (1998) *Appl. Environ. Microbiol. 64(6)*:2158-2165; B.R. Francis *et al.* (1997) *Insect Biochem. Mol. Biol. 27(6)*:541-550; T.P. Keeton *et al.* (1997) *Appl. Environ. Microbiol. 63(9)*:3419-3425; R.K. Vadlamudi *et al.* (1995) *J. Biol. Chem. 270(10)*:5490-5494; Ihara *et al.* (1998) *Comparative Biochem. Physiol. B 120*:197-204; Nagamatsu *et al.* (1998) *Biosci. Biotechnol. Biochem. 62(4)*:727-734, herein incorporated by reference. Such methods could be modified by one of ordinary skill in the art to develop assays utilizing the polypeptides of the invention.

By "cell of interest" is intended any cell in which expression of the polypeptides of the invention is desired. Cells of interest include, but are not limited to mammalian, avian, insect, plant, bacteria, fungi and yeast cells. Cells of interest include but are not limited to cultured cell lines, primary cell cultures, cells *in vivo*, and cells of transgenic organisms.

The methods of the invention encompass using the polypeptides encoded by the nucleotide sequences of the invention in receptor binding and/or toxicity assays to screen candidate ligands and identify novel *Bt* toxin receptor ligands, including receptor agonists and antagonists. Candidate ligands include molecules available from diverse libraries of small molecules created by combinatorial synthetic methods. Candidate ligands also include, but are not limited to antibodies, peptides, and other small molecules designed or deduced to interact with the receptor polypeptides of the invention. Candidate ligands include but are not limited to peptide fragments of the receptor, anti-receptor antibodies, antiidiotypic antibodies mimicking one or more receptor binding domains of a toxin, fusion proteins produced by combining two or more toxins or fragments thereof, and the like. Ligands identified by the screening

methods of the invention include potential novel insecticidal toxins, the insecticidal activity of which can be determined by known methods; for example, as described in U.S. Patent No: 5,407,454; U.S. Application NO: 09/218,942; U.S. Application No: 09/003,217.

The invention provides methods for screening for ligands that bind to the polypeptides described herein. Both the polypeptides and relevant fragments thereof (for example, the toxin binding domain) can be used to screen by assay for compounds that bind to the receptor and exhibit desired binding characteristics. Desired binding characteristics include, but are not limited to binding affinity, binding site specificity, association and dissociation rates, and the like. The screening assays could be intact cell or *in vitro* assays which include exposing a ligand binding domain to a sample ligand and detecting the formation of a ligand-binding polypeptide complex. The assays could be direct ligand-receptor binding assays or ligand competition assays.

In one embodiment, the methods comprise providing at least one *Bt* toxin receptor polypeptide of the invention, contacting the polypeptide with a sample and a control ligand under conditions promoting binding; and determining binding characteristics of sample ligands, relative to control ligands. The methods encompass any method known to the skilled artisan which can be used to provide the polypeptides of the invention in a binding assay. For *in vitro* binding assays, the polypeptide may be provided as isolated, lysed, or homogenized cellular preparations. Isolated polypeptides may be provided in solution, or immobilized to a matrix. Methods for immobilizing polypeptides are well known in the art, and include but are not limited to construction and use of fusion polypeptides with commercially available high affinity ligands. For example, GST fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates. The polypeptides can also be immobilized utilizing well techniques in the art utilizing conjugation of biotin and streptavidin. The polypeptides can also be immobilized utilizing well known techniques in the art utilizing chemical conjugation (linking) of polypeptides to a matrix. Alternatively, the polypeptides may be provided in intact cell binding assays in which the polypeptides are generally expressed as cell surface *Bt* toxin receptors.

The invention provides methods utilizing intact cell toxicity assays to screen for ligands that bind to the receptor polypeptides described herein and confer toxicity upon a

cell of interest expressing the polypeptide. A ligand selected by this screening is a potential insecticidal toxin to insects expressing the receptor polypeptides, particularly enterally. This deduction is premised on theories that insect specificity of a particular Bt toxin is determined by the presence of the receptor in specific insect species, or that binding of the toxins is specific for the receptor of some insect species and is bind is insignificant or nonspecific for other variant receptors. See, for example Hofte *et al* (1989) *Microbiol Rev* 53: 242-255. The toxicity assays include exposing, in intact cells expressing a polypeptide of the invention, the toxin binding domain of the polypeptide to a sample ligand and detecting the toxicity effected in the cell expressing the polypeptide. By "toxicity" is intended the decreased viability of a cell. By "viability" is intended the ability of a cell to proliferate and/or differentiate and/or maintain its biological characteristics in a manner characteristic of that cell in the absence of a particular cytotoxic agent.

In one embodiment, the methods of the present invention comprise providing at least one cell surface *Bt* toxin receptor polypeptide of the invention comprising an extracellular toxin binding domain, contacting the polypeptide with a sample and a control ligand under conditions promoting binding, and determining the viability of the cell expressing the cell surface *Bt* toxin receptor polypeptide, relative to the control ligand.

By "contacting" is intended that the sample and control agents are presented to the intended ligand binding site of the polypeptides of the invention.

By "conditions promoting binding" is intended any combination of physical and biochemical conditions that enables a ligand of the polypeptides of the invention to determinably bind the intended polypeptide over background levels. Examples of such conditions for binding of Cry1 toxins to *Bt* toxin receptors, as well as methods for assessing the binding, are known in the art and include but are not limited to those described in Keeton *et al.* (1998) *Appl Environ Microbiol 64(6)*: 2158-2165; Francis *et al.* (1997) *Insect Biochem Mol Biol 27(6)*:541-550; Keeton *et al.* (1997) *Appl Environ Microbiol 63(9)*:3419-3425; Vadlamudi *et al.* (1995) *J Biol Chem 270(10)*:5490-5494; Ihara *et al.* (1998) *Comparative Biochemistry and Physiology, Part B 120*:197-204; and Nagamatsu *et al.* (1998) *Biosci. Biotechnol. Biochem. 62(4)*:727-734, the contents of which are herein incorporated by reference. In this aspect of the present invention, known and commercially available methods for

studying protein-protein interactions, such as yeast and/or bacterial two-hybrid systems could also be used. Two-hybrid systems are available from, for example, CLONTECH (Palo Alto, Ca) or Display Systems Biotech Inc. (Vista, Ca).

The compositions and screening methods of the invention are useful for designing and developing novel *Bt* toxin receptor ligands including novel insecticidal toxins. Various candidate ligands; ligands screened and characterized for binding, toxicity, and species specificity; and/or ligands having known characteristics and specificities, could be linked or modified to produce novel ligands having particularly desired characteristics and specificities. The methods described herein for assessing binding, toxicity and insecticidal activity could be used to screen and characterize the novel ligands.

In one embodiment of the present invention, the sequences encoding the receptors of the invention, and variants and fragments thereof, are used with yeast and bacterial two-hybrid systems to screen for *Bt* toxins of interest (for example, more specific and/or more potent toxins), or for insect molecules that bind the receptor and can be used in developing novel insecticides.

By "linked" is intended that a covalent bond is produced between two or more molecules. Known methods that can be used for modification and/or linking of polypeptide ligands such as toxins, include but are not limited to mutagenic and recombinogenic approaches including but not limited to site-directed mutagenesis, chimeric polypeptide construction and DNA shuffling. Such methods are described in further detail below. Known polypeptide modification methods also include methods for covalent modification of polypeptides. "Operably linked" means that the linked molecules carry out the function intended by the linkage.

The compositions and screening methods of the present invention are useful for targeting ligands to cells expressing the receptor polypeptides of the invention. For targeting, secondary polyeptides, and/or small molecules which do not bind the receptor polypeptides of the invention are linked with one or more primary ligands which bind the receptor polypeptides; including but not limited to Cry1A toxin; more particularly Cry1 A(b) toxin or a fragment thereof. By this linkage, any polypeptide and/or small molecule linked to a primary ligand could be targeted to the receptor polypeptide, and thereby to a cell expressing the receptor polypeptide; wherein the ligand binding site is available at the extracellular surface of the cell.

In one embodiment of the invention, at least one secondary polypeptide toxin is linked with a primary Cry1 A toxin capable of binding the receptor polypeptides of the invention to produce a combination toxin which is targeted and toxic to insects expressing the receptor for the primary toxin. Such insects include those of the order *lepidoptera*, superfamily *Pyraloidea* and particularly from the species *Ostrinia*, specifically *Ostrinia nubilalis*. Such insects include the lepidopterans *S. frugiperda* and *H. Zea*. Such a combination toxin is particularly useful for eradicating or reducing crop damage by insects which have developed resistance to the primary toxin.

For expression of the *Bt* toxin receptor polypeptides of the invention in a cell of interest, the *Bt* toxin receptor sequences are provided in expression cassettes. The cassette will include 5' and 3' regulatory sequences operably linked to a *Bt* toxin receptor sequence of the invention. In this aspect of the present invention, by "operably linked" is intended a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. In reference to nucleic acids, generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two polypeptide coding regions, contiguous and in the same reading frame. The cassette may additionally contain at least one additional gene to be cotransformed into the organism. Alternatively, the additional gene(s) can be provided on multiple expression cassettes.

Such an expression cassette is provided with a plurality of restriction sites for insertion of the *Bt* toxin receptor sequence to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The expression cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a *Bt* toxin receptor nucleotide sequence of the invention, and a transcriptional and translational termination region functional in host cells. The transcriptional initiation region, the promoter, may be native or analogous, or foreign or heterologous to the plant host. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. By "foreign" is intended that the transcriptional initiation region is not found in the native host cells into which the transcriptional initiation region is introduced. As used

herein, a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

While it may be preferable to express the sequences using heterologous promoters, the native promoter sequences may be used. Such constructs would change expression levels of *Bt* toxin receptor in the cell of interest. Thus, the phenotype of the cell is altered.

The termination region may be native with the transcriptional initiation region, may be native with the operably linked DNA sequence of interest, or may be derived from another source.

Where appropriate, the gene(s) may be optimized for increased expression in a particular transformed cell of interest. That is, the genes can be synthesized using host cell-preferred codons for improved expression.

Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures.

The expression cassettes may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein *et al.* (1989) *PNAS USA 86*:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison *et al.* (1986); MDMV leader (Maize Dwarf Mosaic Virus); *Virology 154*:9-20), and human immunoglobulin heavy-chain binding polypeptide (BiP), (Macejak *et al.* (1991) *Nature 353*:90-94); untranslated leader from the coat polypeptide mRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling *et al.* (1987) *Nature 325*:622-625); tobacco mosaic virus leader (TMV) (Gallie *et al.* (1989) in *Molecular Biology of RNA*, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel *et al.* (1991) *Virology 81*:382-385).

See also, Della-Cioppa *et al.* (1987) *Plant Physiol.* *84*:965-968. Other methods known to enhance translation can also be utilized, for example, introns, and the like.

In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, *in vitro* mutagenesis, primer repair, restriction, annealing, resubstitutions, e.g., transitions and transversions, may be involved.

Using the nucleic acids of the present invention, the polypeptides of the invention could be expressed in any cell of interest, the particular choice of the cell depending on factors such as the level of expression and/or receptor activity desired. Cells of interest include, but are not limited to conveniently available mammalian, plant, insect, bacteria, and yeast host cells. The choice of promoter, terminator, and other expression vector components will also depend on the cell chosen. The cells produce the protein in a non-natural condition (e.g., in quantity, composition, location, and/or time), because they have been genetically altered through human intervention to do so.

It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of a nucleic acid encoding a protein of the present invention. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes will be made.

In brief summary, the expression of isolated nucleic acids encoding a protein of the present invention will typically be achieved by operably linking, for example, the DNA or cDNA to a promoter, followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the DNA encoding a protein of the present invention. To obtain high level expression of a cloned gene, it is desirable to construct expression vectors which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. One

of skill would recognize that modifications can be made to a protein of the present invention without diminishing its biological activity. Some modifications may be made to facilitate the cloning, expression, or incorporation of the targeting molecule into a fusion protein. Such modifications are well known to those of skill in the art and include, for example, a methionine added at the amino terminus to provide an initiation site, or additional amino acids (e.g., poly His) placed on either terminus to create conveniently located restriction sites or termination codons or purification sequences.

Prokaryotic cells may be used as hosts for expression. Prokaryotes most frequently are represented by various strains of *E. coli*; however, other microbial strains may also be used. Commonly used prokaryotic control sequences which are defined herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding site sequences, include such commonly used promoters as the beta lactamase (penicillinase) and lactose (lac) promoter systems (Chang *et al.* (1977) *Nature 198*:1056), the tryptophan (trp) promoter system (Goeddel *et al.* (1980) *Nucleic Acids Res. 8*:4057) and the lambda-derived P L promoter and N-gene ribosome binding site (Shimatake *et al.* (1981) *Nature 292*:128). The inclusion of selection markers in DNA vectors transfected in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol.

The vector is selected to allow introduction into the appropriate host cell. Bacterial vectors are typically of plasmid or phage origin. Appropriate bacterial cells are infected with phage vector particles or transfected with naked phage vector DNA. If a plasmid vector is used, the bacterial cells are transfected with the plasmid vector DNA. Expression systems for expressing a protein of the present invention are available using *Bacillus sp.* and *Salmonella* (Palva *et al.* (1983) *Gene 22*:229-235; Mosbach *et al.* (1983) *Nature 302*:543-545).

A variety of eukaryotic expression systems such as yeast, insect cell lines, plant and mammalian cells, are known to those of skill in the art. The sequences of the present invention can be expressed in these eukaryotic systems. In some embodiments, transformed/transfected plant cells are employed as expression systems for production of the proteins of the instant invention.

Synthesis of heterologous proteins in yeast is well known. Sherman, F. *et al.* (1982) *Methods in Yeast Genetics*, Cold Spring Harbor Laboratory is a well recognized work describing the various methods available to produce the protein in yeast. Two widely utilized yeast for production of eukaryotic proteins are *Saccharomyces cerevisia* and *Pichia pastoris*. Vectors, strains, and protocols for expression in *Saccharomyces* and *Pichia* are known in the art and available from commercial suppliers (e.g., Invitrogen). Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or alcohol oxidase, and an origin of replication, termination sequences and the like as desired.

A protein of the present invention, once expressed, can be isolated from yeast by lysing the cells and applying standard protein isolation techniques to the lysates. The monitoring of the purification process can be accomplished by using Western blot techniques or radioimmunoassay or other standard immunoassay techniques.

The sequences encoding proteins of the present invention can also be ligated to various expression vectors for use in transfecting cell cultures of, for instance, mammalian, insect, or plant origin. Illustrative of cell cultures useful for the production of the peptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the COS, HEK293, BHK21, and CHO cell lines. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase promoter)), an enhancer (Queen *et al.* (1986) *Immunol. Rev. 89*:49), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences. Other animal cells useful for production of proteins of the present invention are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, 1992). A particular example of mammalian cells for expression of a Bt toxin receptor and assessing Bt toxin cytotoxicity mediated by the receptor, includes embryonic 293 cells. See U.S. Patent NO. 5,693,491, herein incorporated by reference.

Appropriate vectors for expressing proteins of the present invention in insect cells are usually derived from the SF9 baculovirus. Suitable insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider *et al.* (1987) *J. Embryol. Exp. Morphol. 27*: 353-365).

As with yeast, when higher animal or plant host cells are employed, polyadenylation or transcription terminator sequences are typically incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague *et al.* (1983) *J. Virol. 45*:773-781). Additionally, gene sequences to control replication in the host cell may be incorporated into the vector such as those found in bovine papilloma virus-type vectors. Saveria-Campo, M., Bovine Papilloma Virus DNA a Eukaryotic Cloning Vector in *DNA Cloning Vol. II a Practical Approach*, D.M. Glover, ed., IRL Pres, Arlington, Virginia pp. 213-238 (1985).

In a particular embodiment of the invention, it may be desirable to negatively control receptor binding; particularly, when toxicity to a cell is no longer desired or if it is desired to reduce toxicity to a lower level. In this case, ligand-receptor polypeptide binding assays can be used to screen for compounds which bind to the receptor but do not confer toxicity to a cell expressing the receptor. The examples of a molecule that can be used to block ligand binding include an antibody that specifically recognizes the ligand binding domain of the receptor such that ligand binding is decreased or prevented as desired.

In another embodiment, receptor polypeptide expression could be blocked by the use of antisense molecules directed against receptor RNA or ribozymes specifically targeted to this receptor RNA. It is recognized that with the provided nucleotide sequences, antisense constructions, complementary to at least a portion of the messenger RNA (mRNA) for the *Bt* toxin receptor sequences can be constructed. Antisense nucleotides are constructed to hybridize with the corresponding mRNA. Modifications of the antisense sequences may be made as long as the sequences hybridize to and interfere with expression of the corresponding mRNA. In this manner, antisense constructions having 70%, preferably 80%, more preferably 85%

sequence similarity to the corresponding antisensed sequences may be used. Furthermore, portions of the antisense nucleotides may be used to disrupt the expression of the target gene. Generally, sequences of at least 50 nucleotides, 100 nucleotides, 200 nucleotides, or greater may be used.

Fragments and variants of the disclosed nucleotide sequences and polypeptides encoded thereby are encompassed by the present invention. By "fragment" is intended a portion of the nucleotide sequence, or a portion of the amino acid sequence, and hence a portion of the polypeptide encoded thereby. Fragments of a nucleotide sequence may encode polypeptide fragments that retain the biological activity of the native polypeptide and, for example, bind *Bt* toxins. Alternatively, fragments of a nucleotide sequence that are useful as hybridization probes generally do not encode fragment polypeptides retaining biological activity. Thus, fragments of a nucleotide sequence may range from at least about 20 nucleotides, about 50 nucleotides, about 100 nucleotides, and up to the full-length nucleotide sequence encoding the polypeptides of the invention.

A fragment of a *Bt* toxin receptor nucleotide sequence that encodes a biologically active portion of a *Bt* toxin receptor polypeptide of the invention will encode at least 15, 25, 30, 50, 100, 150, 200 or 250 contiguous amino acids, or up to the total number of amino acids present in a full-length *Bt* toxin receptor polypeptide of the invention (for example, 1717, 1730, and 1734 amino acids for SEQ ID NOs:2, 4, and 6, respectively. Fragments of a *Bt* toxin receptor nucleotide sequence that are useful as hybridization probes for PCR primers generally need not encode a biologically active portion of a *Bt* toxin receptor polypeptide.

Thus, a fragment of a *Bt* toxin receptor nucleotide sequence may encode a biologically active portion of a *Bt* toxin receptor polypeptide, or it may be a fragment that can be used as a hybridization probe or PCR primer using methods disclosed below. A biologically active portion of a *Bt* toxin receptor polypeptide can be prepared by isolating a portion of one of the *Bt* toxin receptor nucleotide sequences of the invention, expressing the encoded portion of the *Bt* toxin receptor polypeptide (e.g., by recombinant expression *in vitro*), and assessing the activity of the encoded portion of the *Bt* toxin receptor polypeptide. Nucleic acid molecules that are fragments of a *Bt* toxin receptor nucleotide sequence comprise at least 16, 20, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 800, 900, 1,000,

1,100, 1,200, 1,300, or 1,400 nucleotides, or up to the number of nucleotides present in a full-length *Bt* toxin receptor nucleotide sequence disclosed herein (for example, 5498, 5527, and 5614 nucleotides for SEQ ID NOs: 1, 3, and 5, respectively).

By "variants" is intended substantially similar sequences. For nucleotide sequences, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of one of the *Bt* toxin receptor polypeptides of the invention. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis, but which still encode a *Bt* toxin receptor protein of the invention. Generally, variants of a particular nucleotide sequence of the invention will have at least about 40%, 50%, 60%, 65%, 70%, generally at least about 75%, 80%, 85%, preferably at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, and more preferably at least about 98%, 99% or more sequence identity to that particular nucleotide sequence as determined by sequence alignment programs described elsewhere herein using default parameters.

By "variant" protein is intended a protein derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Variant proteins encompassed by the present invention are biologically active, that is they continue to possess the desired biological activity of the native protein, that is, activity as described herein (for example, *Bt* toxin binding activity). Such variants may result from, for example, genetic polymorphism or from human manipulation. Biologically active variants of a native *Bt* toxin receptor protein of the invention will have at least about 40%, 50%, 60%, 65%, 70%, generally at least about 75%, 80%, 85%, preferably at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, and more preferably at least about 98%, 99% or more sequence identity to the amino acid sequence for the native protein as determined by sequence alignment programs described elsewhere herein using default parameters. A biologically active variant of a

protein of the invention may differ from that protein by as few as 1-15 amino acid residues, as few as 1-10, such as 6-10, as few as 5, as few as 4, 3, 2, or even 1 amino acid residue.

The polypeptides of the invention may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the *Bt* toxin receptor polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel (1985) *Proc. Natl. Acad. Sci. USA 82*:488-492; Kunkel *et al.* (1987) *Methods in Enzymol. 154*:367-382; US Patent No. 4,873,192; Walker and Gaastra, eds. (1983) *Techniques in Molecular Biology* (MacMillan Publishing Company, New York) and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff *et al.* (1978) *Atlas of Protein Sequence and Structure* (Natl. Biomed. Res. Found., Washington, D.C.), herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar properties, may be preferable.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the proteins of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to possess the desired toxin binding activity. Obviously, the mutations that will be made in the DNA encoding the variant must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure. See, EP Patent Application Publication No. 75,444.

The deletions, insertions, and substitutions of the protein sequences encompassed herein are not expected to produce radical changes in the characteristics of the protein.

For example, it is recognized that at least about 10, 20, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, and up to 960 amino acids may be deleted from the N-terminus of a polypeptide that has the amino acid sequence set forth in SEQ ID NO:2, and still retain binding function. It is further recognized that at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, and up to

119 amino acids may be deleted from the C-terminus of a polypeptide that has the amino acid sequence set forth in SEQ ID NO:2, and still retain binding function. Deletion variants of the invention that encompass polypeptides having these deletions. It is recognized that deletion variants of the invention that retain binding function encompass polypeptides having these N-terminal or C-terminal deletions, or having any deletion combination thereof at both the C- and the N-termini.

However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays. That is, the activity can be evaluated by receptor binding and/or toxicity assays. See, for example, United States Patent NO: 5,693,491; T.P. Keeton *et al.* (1998) *Appl. Environ. Microbiol. 64(6)*:2158-2165; B.R. Francis *et al.* (1997) *Insect Biochem. Mol. Biol. 27(6)*:541-550; T.P. Keeton *et al.* (1997) *Appl. Environ. Microbiol. 63(9)*:3419-3425; R.K. Vadlamudi *et al.* (1995) *J. Biol. Chem. 270(10)*:5490-5494; Ihara *et al.* (1998) *Comparative Biochem. Physiol. B 120*:197-204; Nagamatsu *et al.* (1998) *Biosci. Biotechnol. Biochem. 62(4)*:727-734, herein incorporated by reference.

Variant nucleotide sequences and polypeptides also encompass sequences and polypeptides derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different toxin receptor coding sequences can be manipulated to create a new toxin receptor, including but not limited to a new *Bt* toxin receptor, possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. For example, using this approach, sequence motifs encoding a domain of interest may be shuffled between the *Bt* toxin receptor gene of the invention and other known *Bt* toxin receptor genes to obtain a new gene coding for a polypeptide with an improved property of interest, such as an increased ligand affinity in the case of a receptor. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA 91*:10747-10751; Stemmer (1994) *Nature 370*:389-391; Crameri *et al.* (1997) *Nature Biotech. 15*:436-438; Moore *et al.* (1997) *J. Mol. Biol. 272*:336-347; Zhang *et al. (1997) Proc. Natl. Acad. Sci. USA 94*:4504-4509; Crameri *et al.* (1998) *Nature 391*:288-291; and U.S. Patent Nos. 5,605,793 and 5,837,448.

Where the receptor polypeptides of the invention are expressed in a cell and associated with the cell membrane (for example, by a transmembrane segment), in order for the receptor of the invention to bind a desired ligand, for example a Cry1 A toxin, the receptor's ligand binding domain must be available to the ligand. In this aspect, it is recognized that the native *Bt* toxin receptor of the invention is oriented such that the toxin binding site is available extracellularly.

Accordingly, in methods comprising use of intact cells, the invention provides cell surface Bt-toxin receptors. By a "cell surface *Bt* toxin receptor" is intended a membrane-bound receptor polypeptide comprising at least one extracellular *Bt* toxin binding site. A cell surface receptor of the invention comprises an appropriate combination of signal sequences and transmembrane segments for guiding and retaining the receptor at the cell membrane such that that toxin binding site is available extracellularly. Where native *Bt* toxin receptors are used for expression, deduction of the composition and configuration of the signal sequences and transmembrane segments is not necessary to ensure the appropriate topology of the polypeptide for displaying the toxin binding site extracellularly. As an alternative to native signal and transmembrane sequences, heterologous signal and transmembrane sequences could be utilized to produce a cell surface receptor polypeptide of the invention.

It is recognized that it may be of interest to generate *Bt* toxin receptors that are capable of interacting with the receptor's ligands intracellularly in the cytoplasm, in the nucleus or other organelles, in other subcellular spaces; or in the extracellular space. Accordingly, the invention encompasses variants of the receptors of the invention, wherein one or more of the segments of the receptor polypeptide is modified to target the polypeptide to a desired intra- or extracellular location.

Also encompassed by the invention are receptor fragments and variants that are useful, among other things, as binding antagonists that will compete with a cell surface receptor of the invention. Such a fragment or variant can, for example, bind a toxin but not be able to confer toxicity to a particular cell. In this aspect, the invention provides secreted receptors, more particularly secreted *Bt* toxin receptors; or receptors that are not membrane bound. The secreted receptors of the invention can contain a heterologous or homologous signal sequence facilitating its secretion from the cell expressing the receptors; and further comprise a secretion variation in the region corresponding to transmembrane segments. By "secretion variation" is intended that amino acids

corresponding to a tranmembrne segment of a membrane bound receptor comprise one or more deletions, substitutions, insertions, or any combination thereof; such that the region no longer retains the requisite hydrophobicity to serve as a transmembrane segment. Sequence alterations to create a secretion variation can be tested by confirming secretion of the polypeptide comprising the variation from the cell expressing the polypeptide.

The polypeptides of the invention can be purified from cells that naturally express it, purified from cells that have been altered to express it (i. e. recombinant) or synthesized using polypeptide synthesis techniques that are well known in the art. In one embodiment, the polypeptide is produced by recombinant DNA methods. In such methods a nucleic acid molecule encoding the polypeptide is cloned into an expression vector as described more fully herein and expressed in an appropriate host cell according to known methods in the art. The polypeptide is then isolated from cells using polypeptide purification techniques well known to those of ordinary skill in the art. Alternatively, the polypeptide or fragment can be synthesized using peptide synthesis methods well known to those of ordinary skill in the art.

The invention also encompasses fusion polypeptides in which one or more polypeptides of the invention are fused with at least one polypeptide of interest. In one embodiment, the invention encompasses fusion polypeptides in which a heterologous polypeptide of interest has an amino acid sequence that is not substantially homologous to the polypeptide of the invention. In this embodiment, the polypeptide of the invention and the polypeptide of interest may or may not be operatively linked. An example of operative linkage is fusion in-frame so that a single polypeptide is produced upon translation. Such fusion polypeptides can, for example, facilitate the purification of a recombinant polypeptide.

In another embodiment, the fused polypeptide of interest may contain a heterologous signal sequence at the N-terminus facilitating its secretion from specific host cells. The expression and secretion of the polypeptide can thereby be increased by use of the heterologous signal sequence.

The invention is also directed to polypeptides in which one or more domains in the polypeptide described herein are operatively linked to heterologous domains having homologous functions. Thus, the toxin binding domain can be replaced with a toxin binding domain for other toxins. Thereby, the toxin specificity of the receptor is based

on a toxin binding domain other than the domain encoded by *Bt* toxin receptor but other characteristics of the polypeptide, for example, membrane localization and topology is based on *Bt* toxin receptor.

Alternatively, the native *Bt* toxin binding domain may be retained while additional heterologous ligand binding domains, including but not limited to heterologous toxin binding domains are comprised by the receptor. Thus, the invention also encompasses fusion polypeptides in which a polypeptide of interest is a heterologous polypeptide comprising a heterologous toxin binding domains. Examples of heterologous polypeptides comprising Cry1 toxin binding domains include, but are not limited to Knight et al (1994) *Mol Micro 11*: 429-436; Lee *et al.* (1996) *Appl Environ Micro 63*: 2845-2849; Gill *et al.* (1995) *J Biol Chem 270*: 27277-27282; Garczynski *et al.* (1991) *Appl Environ Microbiol 10*: 2816-2820; Vadlamudi *et al.* (1995) *J Biol Chem 270(10)*:5490-4, U.S. Patent No5,693,491.

The *Bt* toxin receptor peptide of the invention may also be fused with other members of the cadherin superfamily. Such fusion polypeptides could provide an important reflection of the binding properties of the members of the superfamily. Such combinations could be further used to extend the range of applicability of these molecules in a wide range of systems or species that might not otherwise be amenable to native or relatively homologous polypeptides. The fusion constructs could be substituted into systems in which a native construct would not be functional because of species specific constraints. Hybrid constructs may further exhibit desirable or unusual characteristics otherwise unavailable with the combinations of native polypeptides.

Polypeptide variants encompassed by the present invention include those that contain mutations that either enhance or decrease one or more domain functions. For example, in the toxin binding domain, a mutation may be introduced that increases or decreases the sensitivity of the domain to a specific toxin.

As an alternative to the introduction of mutations, increase in function may be provided by increasing the copy number of ligand binding domains. Thus, the invention also encompasses receptor polypeptides in which the toxin binding domain is provided in more than one copy.

The invention further encompasses cells containing receptor expression vectors comprising the *Bt* toxin receptor sequences, and fragments and variants thereof. The expression vector can contain one or more expression cassettes used to transform a cell

of interest. Transcription of these genes can be placed under the control of a constitutive or inducible promoter (for example, tissue - or cell cycle-preferred).

Where more than one expression cassette utilized, the cassette that is additional to the cassette comprising at least one receptor sequence of the invention, can comprise either a receptor sequence of the invention or any other desired sequences.

The nucleotide sequences of the invention can be used to isolate homologous sequences in insect species other than *ostrinia*, particularly other lepidopteran species, more particularly other *Pyraloidea* species.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller (1988) *CABIOS 4*:11-17; the local homology algorithm of Smith *et al.* (1981) *Adv. Appl. Math. 2*:482; the homology alignment algorithm of Needleman *and Wunsch* (1970) *J. Mol. Biol. 48*:443-453; the search-for-similarity-method of Pearson *and Lipman* (1988) *Proc. Natl. Acad. Sci. 85*:2444-2448; the algorithm of Karlin and Altschul (1990) *Proc.*

Natl. Acad. Sci. USA 872264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA 90*:5873-5877.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0); the ALIGN PLUS program (version 3.0, copyright 1997); and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins *et al.* (1988) *Gene 73*:237-244 (1988); Higgins *et al.* (1989) *CABIOS 5*:151-153; Corpet *et al.* (1988) *Nucleic Acids Res. 16*:10881-90; Huang *et al.* (1992) *CABIOS 8*:155-65; and Pearson *et al.* (1994) *Meth. Mol. Biol. 24*:307-331. The ALIGN and the ALIGN PLUS programs are based on the algorithm of Myers and Miller (1988) *supra*. A PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used with the ALIGN program when comparing amino acid sequences. The BLAST programs of Altschul *et al* (1990) *J. Mol. Biol. 215*:403 are based on the algorithm of Karlin and Altschul (1990) *supra*. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding a protein of the invention. BLAST protein searches can be performed with the BLASTX program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a protein or polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res. 25*:3389. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g., BLASTN for nucleotide sequences, BLASTX for proteins) can be used. See http://www.ncbi.hlm.nih.gov. Alignment may also be performed manually by inspection.

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using GAP Version 10 using the following parameters: % identity using GAP Weight of 50 and Length Weight of 3; % similarity using Gap Weight of 12 and Length Weight of 4, or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

GAP uses the algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48: 443-453, to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty. Default gap creation penalty values and gap extension penalty values in Version 10 of the Wisconsin Genetics Software Package for protein sequences are 8 and 2, respectively. For nucleotide sequences the default gap creation penalty is 50 while the default gap extension penalty is 3. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers consisting of from 0 to 200. Thus, for example, the gap creation and gap extension penalties can be 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or greater.

GAP presents one member of the family of best alignments. There may be many members of this family, but no other member has a better quality. GAP displays four figures of merit for alignments: Quality, Ratio, Identity, and Similarity. The Quality is the metric maximized in order to align the sequences. Ratio is the quality divided by the number of bases in the shorter segment. Percent Identity is the percent of the symbols that actually match. Percent Similarity is the percent of the symbols that are similar. Symbols that are across from gaps are ignored. A similarity is scored when the scoring matrix value for a pair of symbols is greater than or equal to 0.50, the similarity threshold. The scoring matrix used in Version 10 of the

Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70% sequence identity,

preferably at least 80%, more preferably at least 90%, and most preferably at least 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 60%, more preferably at least 70%, 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C lower than the T_m, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid sequence is immunologically cross reactive with the polypeptide encoded by the second nucleic acid sequence.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70% sequence identity to a reference sequence, preferably 80%, more preferably 85%, most preferably at least 90% or 95% sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol. 48*:443-453. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution. Peptides that are "substantially similar" share sequences as noted above except that residue positions that are not identical may differ by conservative amino acid changes.

The nucleotide sequences of the invention can be used to isolate corresponding sequences from other organisms, particularly other insects, more particularly other lepidopteran species. In this manner, methods such as PCR, hybridization, and the like can be used to identify such sequences based on their sequence homology to the sequences set forth herein. Sequences isolated based on their sequence identity to the entire *Bt* toxin receptor sequences set forth herein or to fragments thereof are encompassed by the present invention. Such sequences include sequences that are orthologs of the disclosed sequences. By "orthologs" is intended genes derived from a common ancestral gene and which are found in different species as a result of speciation. Genes found in different species are considered orthologs when their nucleotide sequences and/or their encoded protein sequences share substantial identity as defined elsewhere herein. Functions of orthologs are often highly conserved among species.

In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any organism of interest. Methods for designing PCR primers and PCR cloning are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York). See also Innis *et al.*, eds. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, eds. (1995) *PCR Strategies* (Academic Press, New York); and Innis and Gelfand, eds. (1999) *PCR Methods Manual* (Academic Press, New York). Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially-mismatched primers, and the like.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P, or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the *Bt* toxin receptor sequences of the

invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

For example, the entire *Bt* toxin receptor sequence disclosed herein, or one or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding *Bt* toxin receptor sequences and messenger RNAs. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique among *Bt* toxin receptor sequences and are preferably at least about 10 nucleotides in length, and most preferably at least about 20 nucleotides in length. Such probes may be used to amplify corresponding *Bt* toxin receptor sequences from a chosen plant organism by PCR. This technique may be used to isolate additional coding sequences from a desired organism or as a diagnostic assay to determine the presence of coding sequences in an organism. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, preferably less than 500 nucleotides in length.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of

destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (1984) *Anal. Biochem. 138*:267-284: $T_m = 81.5°C + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% form) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m, hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq$90% identity are sought, the T_m can be decreased 10°C. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature

can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes,* Part I, Chapter 2 (Elsevier, New York); and Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

Thus, isolated sequences that encode for a *Bt* toxin receptor protein and which hybridize under stringent conditions to the *Bt* toxin receptor sequences disclosed herein, or to fragments thereof, are encompassed by the present invention. Such sequences will be at least about 40% to 50% homologous, about 60%, 65%, or 70% homologous, and even at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more homologous with the disclosed sequences. That is, the sequence identity of sequences may range, sharing at least about 40% to 50%, about 60%, 65%, or 70%, and even at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity.

The compositions and screening methods of the invention are useful for identifying cells expressing the BT toxin receptors of the invention, and variants and homologues thereof. Such identification could utilize detection methods at the protein level, such as ligand-receptor binding; or at the nucleotide level. Detection of the polypeptide could be *in situ* by means of *in situ* hybridization of tissue sections but may also be analyzed by bulk polypeptide purification and subsequent analysis by Western blot or immunological assay of a bulk preparation. Alternatively, receptor gene expression can be detected at the nucleic acid level by techniques well known to those of ordinary skill in any art using complimentary polynucleotides to assess the levels of genomic DNA, mRNA, and the like. As an example, PCR primers complimentary to the nucleic acid of interest can be used to identify the level of expression. Tissues and cells identified as expressing the receptor sequences of the invention are determined to be susceptible to toxins which bind the receptor polypeptides.

Where the source of the cells identified to express the receptor polypeptides of the invention is an organism, for example an insect plant pest, the organism is determined to be susceptible to toxins capable of binding the polypeptides. In a

particular embodiment, identification is in a lepidopteran plant pesr expressing the *Bt* toxin receptor of the invention.

The invention encompasses antibody preparations with specificity against the polypeptides of the invention. In further embodiments of the invention, the antibodies are used to detect receptor expression in a cell.

In one aspect, the invention is particularly drawn to compositions and methods for modulating susceptibility of plant pests to *Bt* toxins. However, it is recognized that the methods and compositions could be used for modulating susceptibility of any cell or organism to the toxins. By "modulating" is intended that the susceptibility of a cell or organism to the cytotoxic effects of the toxin is increased or decreased. By "suceptibility" is intended that the viability of a cell contacted with the toxin is decreased. Thus the invention encompasses expressing the cell surface receptor polypeptides of the invention to increase susceptibility of a target cell or organ to *Bt* toxins. Such increases in toxin susceptibility are useful for medical and veterinary purposes in which eradication or reduction of viability of a group of cells is desired. Such increases in susceptibility are also useful for agricultural applications in which eradication or reduction of population of particular plant pests is desired.

Plant pests of interest include, but are not limited to insects, nematodes, and the like. Nematodes include parasitic nematodes such as root-knot, cyst, lesion, and renniform nematodes, etc.

The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

EXAMPLE 1: Isolation of EC *Bt* toxin receptor

Standard recombinant methods well known to those of ordinary skill in the art were carried out. For library construction, total RNA was isolated from the midgut of European corn borer (ECB), *Ostrinia nubilalis*. Corn borer larvae (for example, a mix of stage 2, 3, and 4, equal weight) can be pulverized in liquid nitrogen, homogenized, and total RNA extracted by standard procedures. PolyA RNA can be isolated from the total RNA with standard PolyA isolation procedures, such as the PolyATact system from Promega Corporation, Madison, WI. cDNA synthesis can then be performed and, for example, unidirectional cDNA libraries can be constructed according to known and

commercial procedures, such as the ZAP Express cDNA synthesis kit from Stratagene, La Jolla, CA. cDNA can be amplified by PCR, sized and properly digested with restriction fragments to be ligated into a vector. Subcloned cDNA can be sequenced to identify sequences with the proper peptide to identity corresponding to published sequences. These fragments can be used to probe genomic or cDNA libraries corresponding to a specific host, such as *Ostrinia nubilalis*, to obtain a full length coding sequence. Probes can also be made based on Applicants disclosed sequences. The coding sequence can then be ligated into a desired expression cassette and used to transform a host cell according to standard transformation procedures. Such an expression cassette can be part of a commercially available vector and expression system; for example, the pET system from Novagen Inc. (Madison, WI). Additional vectors that can be used for expression include pBKCMV, pBKRSV, pPbac and pMbac (Stratagene Inc.), pFASTBac1 (Gibco BRL) and other common bacterial, baculovirus, mammalian, and yeast expression vectors.

All vectors were constructed using standard molecular biology techniques as described for example in Sambrook *et al.*, (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory: Cold Spring Harbor, N.Y.).

Expression is tested by ligand blotting and testing for *Bt* toxin binding. Ligand blotting, binding, and toxicity are tested by known methods; for example, as described in Martinez-Ramirez (1994) *Biochem. Biophys. Res. Comm. 201*: 782-787;Vadlamudi *et al.* (1995) *J Biol Chem 270(10)*:5490-4, Keeton *et al.* (1998) *Appl Environ Microbiol 64(6)*:2158-2165; Keeton *et al.* (1997) *Appl Environ Microbiol 63(9)*:3419-3425; Ihara *et al.* (1998) *Comparative Biochemistry and Physiology, Part B 120*:197-204; Nagamatsu *et al.* (1998) *Biosci. Biotechnol. Biochem. 62(4)*:718-726 and Nagamatsu *et al.* (1998) *Biosci. Biotechnol. Biochem. 62(4)*:727-734.

Identifying the CryIA(b) binding polypeptide in ECB was done by ligand blotting brush border membrane vesicle polypeptides and probing those polypeptides for binding with CryIA(b) toxin. Two polypeptides, approximately 210 and 205 kDa, were found to bind to CryIA(b). Blotting and binding were done essentially as described in the preceding paragraph.

Degenerate primers for RT-PCR were designed based on known Cry1 toxin binding polypeptide sequences from *Manducca sexta* and *Bombyx mori*. The primers are shown below. cDNA was constructed from total midgut RNA (cDNA synthesis

kit GibcoBrL). Degenerate primers were used to amplify products of the expected size. The annealing temperature used was 53°C in generation of the 280 bp fragment and 55°C when generating the 1.6 kb fragment.

A 280bp fragment was obtained from ECB midgut RNA. Upon cloning and sequencing, the fragment was identified as having homology with the *Bt* toxin receptor 1 polypeptide (BTR1) described in Vadlamudi *et al.* (1995) *J Biol Chem 270(10)*:5490-4.

A similar approach was used to generate a 1.6 kilobase pair clone. The sequence of primers used to generate the 280 base pair fragment were:

Primer BTRD1S: 5'GTTAMYGTGAGAGAGGCAGAYCC3' (SEQ ID NO:8), and

Primer BTRD5A: 5'GGATRTTAAGMGTCAGYACWCCG3' (SEQ ID NO:9).

The sequence of primers used to generate the 1.6 kb fragment were:

Primer BTRD6S: 5'TCCGAATTCTTCTTYAACCTCATCGAYAACTT3' (SEQ ID NO:10), and

Primer BTRD7A: 5'CGCAAGCTTACTTGGTCGATGTTRCASGTCAT3' (SEQ ID NO:11)

The 1.6 kb fragment clone was ligated in an *E. coli* expression vector, pET-28a-c(+), and expressed using the pET system (Novagen Inc., Madison, WI). Purified polypeptide encoded by this 1.6kb fragment demonstrated binding to CryIA(b) in ligand blots. An ECB midgut cDNA library was generated and screened using this 1.6kb clone, generating 120 positive plaques. Thirty of these plaques were chosen for secondary screening and fifteen of those plaques were purified and sent for DNA sequencing.

The obtained nucleotide sequence of the selected *Bt* toxin receptor clone from ECB is set forth in SEQ ID NO: 1. The total length of the clone is 5498 base pairs. The coding sequences are residues 162-5312. The Cry1A binding site is encoded by residues 4038-4547. The predicted transmembrane domain is encoded by residues 4872-4928. The corresponding deduced amino acid sequence for this *Bt* toxin receptor clone from ECB is set forth in SEQ ID NO: 2.

The purified polypeptide generated from the 1.6kb fragment set forth in SEQ ID NO:7 was used to inoculate rabbits for the production of polyclonal antibodies. On zoo western blots prepared from brush border membrane vesicles from various insect species, this set of antibodies specifically recognized ECB *Bt* toxin receptor

polypeptides, in comparison to *Bt* toxin receptor homologues polypeptides from other insect species. Rabbit polyclonal antibodies were also raised from a purified polypeptide corresponding to amino acids 1293-1462 of SEQ ID NO:2.

Example 2: Isolation of CEW and FAW *Bt* toxin receptor orthologues:

cDNA encoding a full-length *Bt* toxin receptor from corn earworm (CEW, *Heliothis Zea*) was isolated. The nucleotide sequence for this cDNA is set forth in SEQ ID NO: 3. Nucleotides 171-5360 correspond to the open reading frame. Nucleotides 4917-4973 correspond to the transmembrane region. Nucleotides 4083-4589 correspond to the CryIA binding site. The deduced corresponding amino acid sequence for the CEW *Bt* toxin receptor is set forth in SEQ ID NO: 4.

cDNA encoding a full-length *Bt* toxin receptor from fall armyworm (FAW, *Spodoptera frugiperda*) was isolated. The nucleotide sequence for this cDNA is set forth in SEQ ID NO: 5. Nucleotides 162-5363 correspond to the open reading frame. Nucleotides 4110-4616 correspond to the CryIA binding site. Nucleotides 4941-4997 correspond to the transmembrane region. Nucleotides 162-227 correspond to a signal peptide. The deduced corresponding amino acid sequence for the FAW *Bt* toxin receptor is set forth in SEQ ID NO: 6.

Example 3: Binding and cell death in *lepidopteran* insect cells expressing the *Bt* toxin receptors of the invention:

An *in vitro* system is developed to demonstrate the functionality of a *Bt* toxin receptor of the invention. The results disclosed in this example demonstrate that the ECB *Bt* toxin receptor of the invention (SEQ ID NOs:1 and 2) is specifically involved in the binding and killing action of Cry1Ab toxin.

Well known molecular biological methods are used in cloning and expressing the ECB *Bt* toxin receptor in Sf9 cells. A baculovirus expression system (Gibco BRL Catalogue No. 10359-016) is used according to the manufacturer's provided protocols and as described below. *S. frugiperda* (Sf9) cells obtained from ATCC (ATCC-CRL 1711) are grown at 27°C in Sf-900 II serum free medium (Gibco BRL, Catalogue No. 10902-088). These cells, which are not susceptible to Cry1Ab toxin, are transfected with an expression construct (pFastBac1 bacmid, Gibco BRL catalogue NO. 10360-014) comprising an operably linked *Bt* toxin receptor of the invention (SEQ ID NO:1)

downstream of a polyhedrin promoter. Transfected Sf9 cells express the ECB *Bt* toxin receptor and are lysed in the presence of Cry1Ab toxin. Toxin specificities, binding parameters, such as Kd values, and half maximal doses for cellular death and/or toxicity are also determined.

For generating expression constructs, the ECB *Bt* toxin receptor cDNA (SEQ ID NO:1) is subjected to appropriate restriction digestion, and the resulting cDNA comprising the full-length coding region is ligated into the donor plasmid pFastBac1 multiple cloning site. Following transformation and subsequent transposition, recombinant bacmid DNA comprising the ECB *Bt* toxin receptor (RBECB1) is isolated. As a control, recombinant bacmid DNA comprising the reporter gene β-glucuronidase (RBGUS) is similarly constructed and isolated.

For transfection, 2 μg each RBECB1 or RBGUS DNA is mixed with 6 μl of CellFectin (GibcoBRL catalogue NO. 10362-010) in 100 μl of Sf900 medium, and incubated at room temperature for 30 minutes. The mixture is then diluted with 0.8 ml Sf-900 medium. Sf9 cells (10^6/ml per 35 mm well) are washed once with Sf-900 medium, mixed with the DNA/CellFectin mixture, added to the well, and incubated at room temperature for 5 hours. The medium is removed and 2 ml of Sf-900 medium containing penicillin and streptomycin is added to the well. 3-5 days after transfection, Western blotting is used to examine protein expression.

For Western blotting,100 μl of cell lysis buffer (50 mM Tris, pH7.8, 150mM NaCl, 1% Nonidet P-40) is added to the well. The cells are scraped and subjected to 16,000xg centrifugation. Pellet and supernatant are separated and subjected to Western blotting. An antibody preparation against ECB *Bt* toxin receptor (Example 1) is used as first antibody. Alkaline phosphatase-labelled anti-rabbit IgG is used as secondary antibody. Western blot results indicate that the full length ECB *Bt* toxin receptor of the invention (SEQ ID NOs:1 and 2) is expressed in the cell membrane of these cells.

For determining GUS activity, the medium of the cells transfected with RBGUS is removed. The cells and the medium are separately mixed with GUS substrate and assayed for the well known enzymatic activity. GUS activity assays indicate that this reporter gene is actively expressed in the transfected cells.

For determining toxin susceptibility, Cry toxins including but not limited to Cry1A, Cry1B, Cry1C, Cry1D, Cry1E, Cry1F, Cry1I, Cry2, Cry3, and Cry9 toxins

(Schnepf E. *et al.* (1998) Microbiology and *Molecular Biology Reviews 62(3): 775-806*) are prepared by methods known in the art. Crystals are dissolved in pH 10.0, 50 mM carbonate buffer and treated with trypsin. Active fragments of Cry proteins are purified by chromatography. Three to five days after transfection, cells are washed with phosphate buffered saline (PBS). Different concentrations of active fragments of Cry toxins are applied to the cells. At different time intervals, the cells are examined under the microscope to readily determine susceptibility to the toxins. Alternatively, cell death, viability and/or toxicity is quantified by methods well known in the art. See, for example, In Situ Cell Death Detection Kits available from Roche Biochemicals (Catalogue Nos. 2 156 792, 1 684 809, and 1 684 817), and LIVE/DEAD® Viability/Cytotoxicity Kit available from Molecular Probes (catalogue No. L-3224).

A dose-dependent response of RBECB1-transfected cells to Cry1Ab is readily observed, with determined Kd values well within the range for many receptors. Control cells, e.g. those transfected with pFastBac1 bacmid without an insert or those transfected with RBGus are not significantly affected by Cry1Ab. Interaction with other Cry toxins are similarly characterized.

This *in vitro* system is not only be used to verify the functionality of putative *Bt*-toxin receptors, but also used as a tool to determine the active site(s) and other functional domains of the toxin and the receptor. Furthermore, the system is used as a cell-based high throughput screen. For example, methods for distinguishing live versus dead cells by differential dyes are known in the art. This allows for aliquots of transfected cells to be treated with various toxin samples and to serve as a means for screening the toxin samples for desired specificity or binding characteristics. Since the system is used to identify the specificity of Cry protein receptors, it is a useful tool in insect resistance management.

Example 4: Expression of the ECB *Bt* toxin receptor in toxin susceptible stages of the insect's life cycle:

Total RNA was isolated from the eggs, pupae, adults, and the 1st through the 5th instar developmental stages, using TRIzol Reagent (Gibco BRL) essentially as instructed by the manufacturer.(Gibco BRL). The RNA was quantitated and 20 ug of each sample was loaded onto a formaldehyde agarose gel and electrophoresed at

constant voltage. The RNA was then transferred to a nylon membrane via neutral capillary transfer and cross-linked to the membrane using ultraviolet light. For hybridization, a 460 base pair ECB *Bt* toxin receptor DNA probe (bases 3682 to 4141 in SEQ ID NO:1) was constructed from a 460 base pair fragment prepared according to the manufacturer's protocol for Amersham Rediprime II random prime labeling system. The denatured probe was added to the membrane that had been prehybridized for at least 3 hours at 65°C and allowed to incubate with gentle agitation for at least 12 hours at 65°C. Following hybridization, the membranes were washed at 65°C for 1 hour with 1/4X 0.5M NaCl, 0.1M NaPO4 (ph 7.0), 6mM EDTA and 1% SDS solution followed by two 1 hour washes in the above solution without SDS. The membrane was air dried briefly, wrapped in Saran Wrap and exposed to X-ray film.

An ECB *Bt* toxin receptor transcript of 5.5 kilobase was expressed strongly in the larval instars with much reduced expression in the pupal stage. The expression levels appeared to be fairly consistent from first to fifth instar, while decreasing markedly in the pupal stage. There were no detectable transcripts in either the egg or adult stages. These results indicate that the ECB *Bt* toxin transcript is being produced in the susceptible stages of the insects life cycle, while not being produced in stages resistant to the toxic effects of CrylAb.

Example 5: Tissue and subcellular expression of the ECB *Bt* toxin receptor:

Fifth instar ECB were dissected to isolate the following tissues: fat body (FB), malpighian tubules (MT), hind gut (HG), anterior midgut (AM) and posterior midgut (PM). Midguts from fifth instar larvae were also isolated for brush border membrane vesicle (BBMV) preparation using the well known protocol by Wolfersberger *et al.*(1987) *Comp. Biochem. Physiol. 86A*:301-308. Tissues were homogenized in Tris buffered saline, 0.1 % tween-20, centrifuged to pellet insoluble material, and transferred to a fresh tube. 50 ug of protein from each preparation was added to SDS sample buffer and B-mercaptoethanol, heated to 100°C for 10 minutes and loaded onto a 4-12% Bis-Tris gel (Novex). After electrophoresis, the proteins were transferred to a nitrocellulose membrane using a semi-dry apparatus. The membrane was blocked in 5% nonfat dry milk buffer for 1 hour at room temperature with gentle agitation. The primary antibody (Example 1) was added to a final dilution of 1:5000 and allowed to hybridize for 1 hour. The blot was then washed three times for 20

minutes each in nonfat milk buffer. The blot was then hybridized with the secondary antibody (goat anti-rabbit with alkaline phosphatase conjugate) at a dilution of 1:10000 for 1 hour at room temperature. Washes were performed as before. The bands were visualized by using the standard chemiluminescent protocol (Tropix western light protein detection kit).

The ECB *Bt* toxin receptor protein was only visible in the BBMV enriched lane, and not detected in any of the other ECB tissues types. This result indicates that the expression of the ECB *Bt* toxin receptor protein is at very low levels, since the BBMV preparation is a 20-30 fold enriched fraction of the midgut brush border. The result supports propositions that the ECB *Bt* toxin receptor is an integral membrane protein uniquely associated with the brush border. It also demonstrates that the ECB *Bt* toxin receptor is expressed in the envisioned target tissue for CrylAb toxins. However, the result does not necessarily rule out expression in other tissue types, albeit the expression of this protein in those tissues may be lower than in the BBMV enriched fraction.

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

Applicant's or agent's file reference 35718/204291	International application No.

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Name of depository institution
American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Blvd.
Manassas, VA 20110-2209 US

Date of deposit	Accession Number
25 June 1999 (25.06.99)	PTA-278

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THAT WHICH IS CLAIMED:

1. An isolated nucleic acid molecule having a nucleotide sequence encoding a *Bt* toxin receptor, said sequence selected from the group consisting of:

a) a nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5;

b) a nucleotide sequence having at least about 60 % identity to the nucleotide sequence of a);

c) a nucleotide sequence having at least about 70 % identity to the nucleotide sequence of a);

d) a nucleotide sequence having at least about 75 % identity to the nucleotide sequence of a);

e) a nucleotide sequence having at least about 85 % identity to the nucleotide sequence of a);

f) a nucleotide sequence having at least about 95 % identity to the nucleotide sequence of a);

g) a nucleotide sequence consisting of at least 22 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:1;

h) a nucleotide sequence consisting of at least about 15 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:3, or SEQ ID NO:5 ;

i) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of a); and

2. The nucleic acid molecule of claim 1, wherein said toxin is a Cry1A toxin.

3. The nucleic acid of claim 2, wherein said Cry1A toxin is a Cry1A(b) toxin.

4. An isolated polypeptide having the amino acid sequence selected from the group consisting of:

a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

b) an amino acid sequence having at least about 52% identity to

the amino acid sequence set forth in SEQ ID NO: 2;

c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);

d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);

e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);

f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);

g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);

h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);

i) an amino acid sequence encoded by a nucleotide sequence according to claim 1;

j) a variant of the amino acid sequence of a);

k) a fragment of the amino acid sequence of a); and

l) a fragment of the amino acid sequence of a) that binds *Bt* toxin.

5. A fusion polypeptide comprising the polypeptide of claim 4, and at least one polypeptide of interest.

6. The fusion polypeptide of claim 5, wherein said polypeptide of interest is a toxin receptor.

7. An expression cassette comprising a nucleotide sequence encoding the fusion polypeptide of claim 5, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a cell of interest.

8. The expression cassette of claim 7 wherein said polypeptide of interest is a toxin receptor.

9. An antibody preparation specific for the polypeptide of claim 4.

10. An expression cassette comprising at least one nucleotide sequence according to claim 1, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a cell of interest.

11. The expression cassette of claim 10, wherein said cell of interest is an insect or mammalian cell.

12. The expression cassette of claim 10 wherein said cell of interest is a microorganism.

13. The expression cassette of claim 12 wherein said microorganism is yeast or bacteria.

14. A vector for delivery of a nucleotide sequence to a cell of interest, the vector comprising at least one nucleotide sequence according to claim 1.

15. A cell containing the vector of claim 14.

16. A transformed cell of interest having stably incorporated within its genome a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5;

b) a nucleotide sequence having at least about 60 % identity to the nucleotide sequence of a);

c) a nucleotide sequence having at least about 70 % identity to the nucleotide sequence of a);

d) a nucleotide sequence having at least about 75 % identity to the nucleotide sequence of a);

e) a nucleotide sequence having at least about 85 % identity to the nucleotide sequence of a);

f) a nucleotide sequence having at least about 95 % identity to the nucleotide sequence of a);

g) a nucleotide sequence consisting of at least 22 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:1;

h) a nucleotide sequence consisting of at least about 15 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:3, or SEQ ID NO:5 ;

i) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of a); and

17. The transformed cell of claim 16 , wherein said cell is a plant cell.

18. The transformed cell of claim 17, wherein said plant cell is monocotyledonous.

19. A method for screening for ligands that bind *Bt* toxin receptor, said method comprising:

i) providing at least one *Bt* toxin receptor polypeptide according to claim 4;

ii) contacting said polypeptide with a sample and a control ligand under conditions promoting binding; and

iii) determining binding characteristics of said sample ligand, relative to said control ligand.

20. A method for screening for ligands that bind *Bt* toxin receptor, said method comprising:

i) providing at least one *Bt* toxin receptor polypeptide having the amino acid sequence selected from the group consisting of a, b, c, d, e, f, g, h , i, and j of claim 4 in cells expressing said polypeptide wherein said polypyptide comprises a toxin binding domain ;

ii) contacting said cells with a sample and a control ligand under conditions promoting binding; and

iii) determining binding characteristics of said sample ligand, relative to said control ligand.

21. The method of claim 20 wherein said toxin is a Cry1A toxin.

22. A method for screening for toxins that bind Bt toxin receptor, said method comprising the steps of claim 20; further comprising determining viability of said cells contacted with a sample ligand relative to said cells contacted with a control ligand.

23. The method of claim 20, wherein said sample ligand is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having the amino acid sequence selected from the group consisting of:

a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;

c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);

d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);

e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);

f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);

g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);

h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);

i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5; and

j) a variant of the amino acid sequence of a).

24. The method of claims 21, wherein said sample ligand is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having the amino acid sequence selected from the group consisting of:

a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;

c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);

d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);

e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);

f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);

g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);

h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);

i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5; and

j) a variant of the amino acid sequence of a).

25. The method of claims 22, wherein said sample ligand is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having the amino acid sequence selected from the group consisting of:

a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;

c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);

d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);

e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);

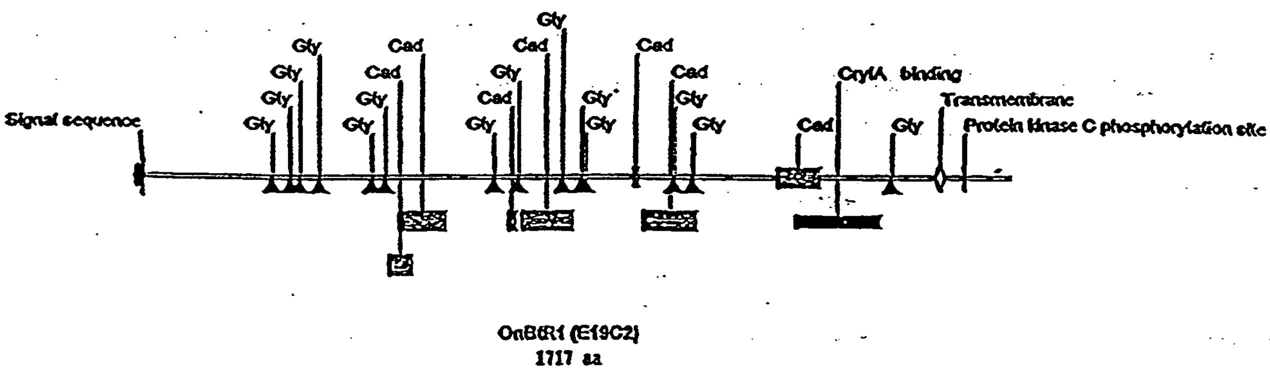
f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);

g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);

h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);

i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5; and

j) a variant of the amino acid sequence of a).



Gly = putative glycosilation sites

Cad = cadherin-like domain

FIGURE 1

SEQUENCE LISTING

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Mathis, John P.
Meyer, Terry E.

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Lepidopteran Insects and Methods of Use

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Arg Ala His Phe Ile Arg Asp Asn Val Pro Val Gln Ala Gln Glu Val
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Asp Tyr Phe Pro Pro Gly Asp Thr Asp Ser Ser Ser Gly Ile Val Leu
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His Met Gly Glu Ala Thr Asp Asn Lys Pro Val Thr Thr His Gly Asn
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Trp Ser Glu Gln Pro Leu Ile Pro Gly Pro Thr Arg Glu Glu Val Cys
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Met Glu Asn Phe Leu Pro Asp Gln Met Ile Gln Val Ile Tyr Met Glu
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Glu Glu Ile Glu Gly Asp Val Ile Ile Ala Lys Leu Asn Tyr Gln Gly
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Ser Asn Thr Pro Val Leu Ser Ile Met Ser Gly Gln Pro Arg Ala Gln
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Leu Gly Pro Glu Phe Arg Gln Asn Glu Ala Asp Gly Gln Trp Ser Leu
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Val Ile Thr Gln Arg Gln Asp Tyr Glu Thr Ala Thr Met Gln Ser Tyr
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Leu Glu Ile Val Asn Ile Asp Asp Asn Pro Pro Ile Leu Gln Val Val
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Ser Ala Cys Val Ile Pro Glu His Gly Glu Ala Arg Leu Thr Asp Cys
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Val Tyr Gln Val Ser Asp Arg Asp Gly Glu Ile Ser Thr Arg Phe Met
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Met Val Gly Glu Tyr Asp Pro Ser Asp Trp Phe Asn Met Lys Met Thr
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Val Gly Ile Asn Ser Pro Leu Asn Phe Glu Thr Thr Gln Leu His Ile
245 250 255
Phe Ser Val Thr Ala Ser Asp Ser Leu Pro Asn Asn His Thr Val Thr
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Met Met Val Gln Val Glu Asn Val Glu Ser Arg Pro Pro Arg Trp Val
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Ser Leu Arg Ala Ile Asp Gly Asp Thr Gly Ile Asn Arg Ala Ile Asn
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Tyr Thr Leu Ile Arg Asp Asp Ala Asp Asp Phe Phe Ser Leu Glu Val
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Asp Ala Ser Phe Ala Thr Glu Ala His Ile Phe Ile Ile Val Asn Asp
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Glu Asp Val Phe Pro Pro Gly Ala Ala Ser Ala Phe Tyr Ile Ala Pro
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Asp Val Asn Asn Thr Pro Pro Thr Leu Arg Leu Pro Arg Ser Thr Pro
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Tyr Thr Val Ile Ala Ser Asp Glu Cys Ser Leu Glu Asn Arg Thr Glu
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Cys Pro Pro Asp Ser Asn Tyr Phe Glu Val Pro Gly Asp Ile Glu Ile
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Glu Ile Ile Asp Thr Asn Asn Lys Val Pro Glu Pro Leu Thr Glu Lys
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Asp His Gly Tyr Pro Gln Gln Arg Ser Asn Glu Thr Tyr Thr Leu Val
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Pro Leu Trp Thr Asp Val Thr Phe Ser Val Val Phe Val Pro Thr Gln
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Tyr Thr Leu His Ile Ala Ala Ser Asn Ser Pro Asp Ala Thr Gly Ile
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His Gly Met Phe Glu Phe Asp Val Ile Ala Thr Asp Thr Ala Ser Ala
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Ile Asp Thr Ala Arg Val Lys Val Tyr Leu Ile Ser Ser Gln Asn Arg
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Val Thr Phe Ile Phe Asp Asn Gln Leu Glu Thr Val Glu Gln Asn Arg
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Asn Phe Ile Ala Ala Thr Phe Ser Thr Gly Phe Asn Met Thr Cys Asn
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Val Thr Gly Asp Thr Pro Thr Leu Gly Glu Glu Ser Met Gln Ile Ala
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Val Tyr Ala Leu Ala Ala Leu Ser Ala Val Leu Gly Phe Leu Cys Leu
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Val Leu Leu Leu Ala Leu Phe Cys Arg Thr Arg Ala Leu Asn Arg Gln
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Ser Asn Pro Met Trp Asn Glu Ala Ile Arg Ala Pro Asp Phe Asp Ala
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Leu Thr Phe Ala Gln Asp Cys Ser Tyr Met Val Ala Ile Pro Arg Pro
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Arg Tyr Pro Leu Ile Pro Val Glu Gly Arg Glu Asp Val Cys Met Asn
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Glu Glu Ile Glu Gly Asp Val Ala Ile Ala Arg Leu Asn Tyr Arg Gly
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485 490 495

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580 585 590

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Val Gln Ile Pro Ala Asp Asp Thr Leu Gly Glu Pro Tyr Asn Thr Asn
595 600 605 610

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Thr Thr Gln Leu Val Ile Lys Leu Arg Asp Ile Asn Asn Thr Pro Pro
615 620 625

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Val Ile Gly Glu Asp His Asp Ile Ser Thr Phe Thr Ile Thr Ile Ile
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Tyr Glu Gly Ala Asp Asp Gly Gln His Val Val Gln Ile Tyr Ala Ser
    900                     905                     910

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Asp Leu Asp Arg Asp Glu Ile Tyr His Lys Val Ser Tyr Gln Ile Asn
915                     920                     925                 930

tac gcg atc aac tct cgt ctc cgc gac ttc ttc gag atg gac ctg gag      3008
Tyr Ala Ile Asn Ser Arg Leu Arg Asp Phe Phe Glu Met Asp Leu Glu
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Ser Gly Leu Val Tyr Val Asn Asn Thr Ala Gly Glu Leu Leu Asp Arg
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Asp Gly Asp Glu Pro Thr His Arg Ile Phe Phe Asn Val Ile Asp Asn
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ttc tat gga gaa gga gat ggc aac cgc aat cag aac gag aca caa gtg      3152
Phe Tyr Gly Glu Gly Asp Gly Asn Arg Asn Gln Asn Glu Thr Gln Val
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Leu Val Val Leu Leu Asp Ile Asn Asp Asn Tyr Pro Glu Leu Pro Glu
995                     1000                    1005                1010

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Thr Ile Pro Trp Ala Ile Ser Glu Ser Leu Glu Leu Gly Glu Arg Val
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Gln Pro Glu Ile Phe Ala Arg Asp Arg Asp Glu Pro Gly Thr Asp Asn
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Ser Arg Val Ala Tyr Ala Ile Thr Gly Leu Ala Ser Thr Asp Arg Asp
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Ile Gln Val Pro Asn Leu Phe Asn Met Ile Thr Ile Glu Arg Asp Arg
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Tyr Trp Gly Thr Tyr Gln Ile Asp Ile Gln Ala Tyr Asp His Gly Ile
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Gly Glu His Phe Thr Val Asp Pro Arg Thr Asn Val Leu Ser Leu Val
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Lys Pro Leu Asp Arg Ser Glu Gln Glu Thr His Thr Leu Ile Ile Gly
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Thr Val Thr Val Asn Val Arg Glu Ala Asn Pro Arg Pro Val Phe Gln
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Arg Ala Leu Tyr Thr Ala Gly Ile Ser Ala Gly Asp Phe Ile Glu Arg
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Asn Leu Leu Thr Leu Val Ala Thr His Ser Glu Asp Leu Pro Ile Thr
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Tyr Thr Leu Ile Gln Glu Ser Met Glu Ala Asp Pro Thr Leu Glu Ala
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Thr Ala Phe Phe Gly Met Thr Cys Asn Ile Asp Gln Ser Trp Trp Ala
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Tyr Asp Ser Asp Leu Ile Gly Ile Glu Asp Leu Pro Gln Phe Arg Asn
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Asp Tyr Phe Pro Pro Glu Glu Gly Ser Ser Met Arg Gly Val Val Asn
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Trp Ser Arg Tyr Pro Leu Ile Pro Val Glu Gly Arg Glu Asp Val Cys
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Met Glu Glu Glu Ile Glu Gly Asp Val Ala Ile Ala Arg Leu Asn Tyr
85 90 95
Arg Gly Thr Asn Thr Pro Thr Ile Val Ser Pro Phe Ser Phe Gly Thr
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Phe Asn Met Leu Gly Pro Val Ile Arg Arg Ile Pro Glu Asn Gly Gly
115 120 125
Asp Trp His Leu Val Ile Thr Gln Arg Gln Asp Tyr Glu Thr Pro Gly
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Met Gln Gln Tyr Ile Phe Asp Val Arg Val Asp Asp Glu Pro Leu Val
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Ala Thr Val Met Leu Leu Ile Val Asn Ile Asp Asp Asn Asp Pro Ile
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Ile Gln Met Phe Glu Pro Cys Asp Ile Pro Glu Arg Gly Glu Thr Gly
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Ile Thr Ser Cys Lys Tyr Thr Val Ser Asp Ala Asp Gly Glu Ile Ser
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Thr Arg Phe Met Arg Phe Glu Ile Ser Ser Asp Arg Asp Asp Glu

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His Met Arg Val His Val Lys Lys Pro Leu Asp Tyr Glu Glu Asn Pro
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Leu His Leu Phe Arg Val Thr Ala Tyr Asp Ser Leu Pro Asn Thr His
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Thr Val Thr Met Met Val Gln Val Glu Asn Val Glu Asn Arg Pro Pro
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Arg Trp Met Glu Ile Phe Ala Val Gln Gln Phe Asp Glu Lys Thr Glu
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Gln Ser Phe Arg Val Arg Ala Ile Asp Gly Asp Thr Gly Ile Asp Lys
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Pro Ile Phe Tyr Arg Ile Glu Thr Glu Lys Gly Glu Glu Asp Leu Phe
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Ser Ile Gln Thr Ile Glu Gly Gly Arg Glu Gly Ala Trp Phe Asn Val
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Ala Pro Ile Asp Arg Asp Thr Leu Glu Lys Glu Val Phe His Val Ser
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Ile Ile Ala Tyr Lys Tyr Gly Asp Asn Asp Val Glu Gly Ser Ser Ser
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Phe Gln Ser Lys Thr Asp Val Val Ile Ile Val Asn Asp Val Asn Asp
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Glu Thr Ala Met Thr Leu Asn Leu Glu Asp Phe Gly Phe His Asp Arg
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Asp Leu Gly Pro His Ala Gln Tyr Thr Val His Leu Glu Ser Ile His
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Pro Pro Arg Ala His Glu Ala Phe Tyr Ile Ala Pro Glu Val Gly Tyr
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Gln Arg Gln Ser Phe Ile Met Gly Thr Gln Asn His His Met Leu Asp
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Asp Met Asp Asp Pro Lys Trp Val Gly Ile Ala Ile Ile Asn Ile Lys
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Val Pro Asp Gly Phe Val Ile Pro Thr Gln Leu His Ala Thr Asp Pro
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Gly Ser Val Leu Ala Thr Asp Ile Asp Gly Pro Leu Tyr Asn Gln Val
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Arg Tyr Thr Ile Thr Pro Arg Leu Asp Thr Pro Glu Asp Leu Val Asp
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Ile Asp Phe Asn Thr Gly Gln Ile Ser Val Lys Leu His Gln Ala Ile
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Asp Ala Asp Glu Pro Pro Arg Gln Asn Leu Tyr Tyr Thr Val Ile Ala
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Ser Asp Lys Cys Asp Leu Leu Thr Val Thr Glu Cys Pro Pro Asp Pro
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Tyr Ile Tyr Glu Gly Ala Asp Asp Gly Gln His Val Val Gln Ile Tyr
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Ala Ser Asp Leu Asp Arg Asp Glu Ile Tyr His Lys Val Ser Tyr Gln
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Pro Tyr Asn Phe His Asp Pro Val Phe Val Phe Pro Gln Pro Gly Ser
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Pro Asp Pro Trp Ser Asn Asn His Gly Asp Gln Arg Ile Tyr Met Glu
70                  75                  80                  85

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Glu Glu Ile Glu Gly Pro Val Val Ile Ala Lys Ile Asn Tyr Gln Gly
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Ile Phe Arg Val Thr Ala Ser Asp Ser Leu Pro Asn Asn Arg Thr Val
            265                 270                 275

gtc atg atg gtt gaa gta gag aac gtg gaa cat aga aat cct cgg tgg     1040
Val Met Met Val Glu Val Glu Asn Val Glu His Arg Asn Pro Arg Trp
        280                 285                 290

atg gag atc ttt gct gtg caa cag ttt gat gaa aaa cag gcg aaa tcg     1088
Met Glu Ile Phe Ala Val Gln Gln Phe Asp Glu Lys Gln Ala Lys Ser
    295                 300                 305

ttc aca gtg cga gct att gat ggc gac acg gga atc aat aaa cct ata     1136
Phe Thr Val Arg Ala Ile Asp Gly Asp Thr Gly Ile Asn Lys Pro Ile
310                 315                 320                 325

ttc tat cgt ata gaa act gaa gat gaa gac aaa gag ttc ttc agc att     1184
Phe Tyr Arg Ile Glu Thr Glu Asp Glu Asp Lys Glu Phe Phe Ser Ile
                330                 335                 340

gag aac ata ggg gaa ggc aga gac ggt gcc aga ttc cac gtg gct cct     1232
Glu Asn Ile Gly Glu Gly Arg Asp Gly Ala Arg Phe His Val Ala Pro
            345                 350                 355

ata gac aga gac tac ctg aaa agg gat atg ttt cat ata aga ata att     1280
Ile Asp Arg Asp Tyr Leu Lys Arg Asp Met Phe His Ile Arg Ile Ile
        360                 365                 370

gca tat aaa caa ggt gat aat gac aaa gaa ggt gaa tca tcg ttc gag     1328
Ala Tyr Lys Gln Gly Asp Asn Asp Lys Glu Gly Glu Ser Ser Phe Glu
    375                 380                 385

acc tca gca aat gtg acg att ata att aac gat ata aat gat cag agg     1376
Thr Ser Ala Asn Val Thr Ile Ile Ile Asn Asp Ile Asn Asp Gln Arg
390                 395                 400                 405

cca gaa ccc ttc cat aaa gaa tac acg atc tcc ata atg gaa gaa act     1424
Pro Glu Pro Phe His Lys Glu Tyr Thr Ile Ser Ile Met Glu Glu Thr
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                410                 415                 420

gcg atg acc tta gat ttg caa gag ttt ggt ttc cat gac cgt gac att     1472
Ala Met Thr Leu Asp Leu Gln Glu Phe Gly Phe His Asp Arg Asp Ile
            425                 430                 435

ggt ccc cac gct cag tac gac gtt cac tta gag agt ata cag cca gag     1520
Gly Pro His Ala Gln Tyr Asp Val His Leu Glu Ser Ile Gln Pro Glu
        440                 445                 450

ggg gcc cat acc gct ttc tac atc gcc cct gaa gaa ggt tac cag gcc     1568
Gly Ala His Thr Ala Phe Tyr Ile Ala Pro Glu Glu Gly Tyr Gln Ala
    455                 460                 465

cag tct ttc acc ata ggt act aga atc cat aac atg ttg gat tat gaa     1616
Gln Ser Phe Thr Ile Gly Thr Arg Ile His Asn Met Leu Asp Tyr Glu
470                 475                 480                 485

gat gac gac tac aga cca gga ata aag cta aag gca gta gca att gac     1664
Asp Asp Asp Tyr Arg Pro Gly Ile Lys Leu Lys Ala Val Ala Ile Asp
                490                 495                 500

aga cac gat aac aat cac att ggg gaa gca att att aac att aac ctt     1712
Arg His Asp Asn Asn His Ile Gly Glu Ala Ile Ile Asn Ile Asn Leu
            505                 510                 515

atc aat tgg aat gat gag cta cct ata ttc gac gag gac gcc tac aac     1760
Ile Asn Trp Asn Asp Glu Leu Pro Ile Phe Asp Glu Asp Ala Tyr Asn
        520                 525                 530

gtg aca ttt gag gag acg gtc ggt gat ggc ttc cac att ggt aaa tac     1808
Val Thr Phe Glu Glu Thr Val Gly Asp Gly Phe His Ile Gly Lys Tyr
    535                 540                 545

cgg gct aaa gac aga gac atc ggt gac ata gtc gag cac tcg ata ttg     1856
Arg Ala Lys Asp Arg Asp Ile Gly Asp Ile Val Glu His Ser Ile Leu
550                 555                 560                 565

ggc aac gct gca aac ttc ctg aga att gac ata gat act gga gat gtg     1904
Gly Asn Ala Ala Asn Phe Leu Arg Ile Asp Ile Asp Thr Gly Asp Val
                570                 575                 580

tac gtg tca cgg gac gat tac ttt gat tat caa aga cag aac gaa atc     1952
Tyr Val Ser Arg Asp Asp Tyr Phe Asp Tyr Gln Arg Gln Asn Glu Ile
            585                 590                 595

ata gtt cag att ctg gct gtt gat aca cta ggt tta cct cag aac agg     2000
Ile Val Gln Ile Leu Ala Val Asp Thr Leu Gly Leu Pro Gln Asn Arg
        600                 605                 610

gct acc aca cag ctc acg ata ttt ttg gaa gac atc aac aac acg cca     2048
Ala Thr Thr Gln Leu Thr Ile Phe Leu Glu Asp Ile Asn Asn Thr Pro
    615                 620                 625

cct ata ctg cga ctg cca cgt tcc agt cca agt gta gaa gag aac gtt     2096
Pro Ile Leu Arg Leu Pro Arg Ser Ser Pro Ser Val Glu Glu Asn Val
630                 635                 640                 645

gaa gtc ggg cac ccg att acc gag ggg cta acg gcg aca gac cca gac     2144
Glu Val Gly His Pro Ile Thr Glu Gly Leu Thr Ala Thr Asp Pro Asp
                650                 655                 660
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acc aca gcc gat tta cac ttc gag atc gat tgg gac aat tct tac gct      2192
Thr Thr Ala Asp Leu His Phe Glu Ile Asp Trp Asp Asn Ser Tyr Ala
            665                 670                 675

acg aag cag ggc acc aat gga ccc aac act gca gac tac cac gga tgc      2240
Thr Lys Gln Gly Thr Asn Gly Pro Asn Thr Ala Asp Tyr His Gly Cys
        680                 685                 690

gta gaa atc ctg acg gta tac cca gat cct gac aat cac ggg aga gct      2288
Val Glu Ile Leu Thr Val Tyr Pro Asp Pro Asp Asn His Gly Arg Ala
    695                 700                 705

gag ggt cac ttg gtg gca cgt gag gtc agt gat ggc gtg acc atc gat      2336
Glu Gly His Leu Val Ala Arg Glu Val Ser Asp Gly Val Thr Ile Asp
710                 715                 720                 725

tac gag aag ttt gag gtg ctg tac ctc gtc gtc agg gtg ata gat cgc      2384
Tyr Glu Lys Phe Glu Val Leu Tyr Leu Val Val Arg Val Ile Asp Arg
                730                 735                 740

aac act gtc att ggc cct gat tat gac gaa gca atg ctg acg gtg acg      2432
Asn Thr Val Ile Gly Pro Asp Tyr Asp Glu Ala Met Leu Thr Val Thr
            745                 750                 755

ata atc gat atg aac gac aac tgg ccg ata tgg gcc gac aac acg ctg      2480
Ile Ile Asp Met Asn Asp Asn Trp Pro Ile Trp Ala Asp Asn Thr Leu
        760                 765                 770

cag cag aca ctg cgc gtg cgc gag atg gcc gac gaa gga gtc atc gtc      2528
Gln Gln Thr Leu Arg Val Arg Glu Met Ala Asp Glu Gly Val Ile Val
    775                 780                 785

ggt aca ctg ctc gcc acc gac ttg gat ggc cct ctc tac aac cga gtc      2576
Gly Thr Leu Leu Ala Thr Asp Leu Asp Gly Pro Leu Tyr Asn Arg Val
790                 795                 800                 805

cgc tac acc atg gtc ccc atc aag gac act cct gat gac cta ata gcg      2624
Arg Tyr Thr Met Val Pro Ile Lys Asp Thr Pro Asp Asp Leu Ile Ala
                810                 815                 820

atc aac tac gtc acc ggt cag ctg act gtg aac aag ggg caa gca att      2672
Ile Asn Tyr Val Thr Gly Gln Leu Thr Val Asn Lys Gly Gln Ala Ile
            825                 830                 835

gac gca gat gat cca cct cgc ttc tac ctg tat tac aag gtc act gcc      2720
Asp Ala Asp Asp Pro Pro Arg Phe Tyr Leu Tyr Tyr Lys Val Thr Ala
        840                 845                 850

agc gat aag tgc tct ctt gac gag ttc ttc cct gtg tgc cca cct gac      2768
Ser Asp Lys Cys Ser Leu Asp Glu Phe Phe Pro Val Cys Pro Pro Asp
    855                 860                 865

ccc act tac tgg aat acc gag gga gag ata gcg atc gcg ata acc gat      2816
Pro Thr Tyr Trp Asn Thr Glu Gly Glu Ile Ala Ile Ala Ile Thr Asp
870                 875                 880                 885

acg aac aac aaa att cca cgc gcg gaa aca gat atg ttc cct agt gaa      2864
Thr Asn Asn Lys Ile Pro Arg Ala Glu Thr Asp Met Phe Pro Ser Glu
                890                 895                 900

aag cgc atc tat gag aac aca ccc aat ggt acc aag atc acg acg atc      2912
Lys Arg Ile Tyr Glu Asn Thr Pro Asn Gly Thr Lys Ile Thr Thr Ile
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          905                      910                      915

atc gct agt gac cag gac aga gat cga cca aat aac gcg ctg acg tac      2960
Ile Ala Ser Asp Gln Asp Arg Asp Arg Pro Asn Asn Ala Leu Thr Tyr
        920                     925                     930

aga atc aac tac gca ttc aac cac agg ctg gag aac ttc ttc gca gtg      3008
Arg Ile Asn Tyr Ala Phe Asn His Arg Leu Glu Asn Phe Phe Ala Val
    935                     940                     945

gac cct gat act ggt gaa ctg ttt gtc cac ttc acc act agc gaa gtg      3056
Asp Pro Asp Thr Gly Glu Leu Phe Val His Phe Thr Thr Ser Glu Val
950                     955                     960                     965

ttg gac aga gac gga gag gaa ccg gag cat agg atc atc ttc acc atc      3104
Leu Asp Arg Asp Gly Glu Glu Pro Glu His Arg Ile Ile Phe Thr Ile
                970                     975                     980

gtc gat aac ttg gaa ggc gct gga gat ggc aat cag aac aca atc tcc      3152
Val Asp Asn Leu Glu Gly Ala Gly Asp Gly Asn Gln Asn Thr Ile Ser
            985                     990                     995

acg gag gtg cgt gtt ata ctg ctt gat ata aac gac aat aag ccg gaa      3200
Thr Glu Val Arg Val Ile Leu Leu Asp Ile Asn Asp Asn Lys Pro Glu
        1000                    1005                    1010

cta cca att cct gat ggc gaa ttt tgg acc gtt tcc gaa ggt gaa gtg      3248
Leu Pro Ile Pro Asp Gly Glu Phe Trp Thr Val Ser Glu Gly Glu Val
    1015                    1020                    1025

gag gga aaa cgc att cca cca gag att cac gca cac gac aga gat gaa      3296
Glu Gly Lys Arg Ile Pro Pro Glu Ile His Ala His Asp Arg Asp Glu
1030                    1035                    1040                    1045

cca ttc aac gac aac tct cgc gtg gga tat gaa att cga tcg atc aaa      3344
Pro Phe Asn Asp Asn Ser Arg Val Gly Tyr Glu Ile Arg Ser Ile Lys
                1050                    1055                    1060

ttg atc aat aga gac atc gag ctt cct caa gat cca ttc aaa ata ata      3392
Leu Ile Asn Arg Asp Ile Glu Leu Pro Gln Asp Pro Phe Lys Ile Ile
            1065                    1070                    1075

acg att gat gat ctc gat acc tgg aaa ttc gtt gga gag ttg gag act      3440
Thr Ile Asp Asp Leu Asp Thr Trp Lys Phe Val Gly Glu Leu Glu Thr
        1080                    1085                    1090

acc atg gac ctt aga gga tac tgg gga acc tat gat gtc gag ata cgt      3488
Thr Met Asp Leu Arg Gly Tyr Trp Gly Thr Tyr Asp Val Glu Ile Arg
    1095                    1100                    1105

gcg ttt gac cac ggt ttc ccg atg ctg gat tca ttc gag acc tac caa      3536
Ala Phe Asp His Gly Phe Pro Met Leu Asp Ser Phe Glu Thr Tyr Gln
1110                    1115                    1120                    1125

cta acc gtc agg cca tac aac ttc cat tca ccg gtg ttt gtg ttc cca      3584
Leu Thr Val Arg Pro Tyr Asn Phe His Ser Pro Val Phe Val Phe Pro
                1130                    1135                    1140

act cct ggc tca acc atc agg ctt tct agg gag cgt gct ata gtc aat      3632
Thr Pro Gly Ser Thr Ile Arg Leu Ser Arg Glu Arg Ala Ile Val Asn
            1145                    1150                    1155
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ggt atg ctg gct ctg gct aat atc gcg agc gga gag ttc ctc gac aga     3680
Gly Met Leu Ala Leu Ala Asn Ile Ala Ser Gly Glu Phe Leu Asp Arg
        1160                1165                1170

ctc tct gcc act gat gaa gat ggg cta cac gca ggc aga gta act ttc     3728
Leu Ser Ala Thr Asp Glu Asp Gly Leu His Ala Gly Arg Val Thr Phe
    1175                1180                1185

tcc ata gct gga aac gat gaa gct gcg gaa tat ttc aat gtg ttg aac     3776
Ser Ile Ala Gly Asn Asp Glu Ala Ala Glu Tyr Phe Asn Val Leu Asn
1190                1195                1200                1205

gac ggt gac aac tca gca atg ctc acg ctg aag caa gca ttg ccc gct     3824
Asp Gly Asp Asn Ser Ala Met Leu Thr Leu Lys Gln Ala Leu Pro Ala
                1210                1215                1220

ggc gtc cag cag ttt gag ttg gtt att cgg gcc acg gac ggc ggg acg     3872
Gly Val Gln Gln Phe Glu Leu Val Ile Arg Ala Thr Asp Gly Gly Thr
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gag ccg gga cct agg agt acc gac tgc tcc gtc act gtg gtg ttt gtg     3920
Glu Pro Gly Pro Arg Ser Thr Asp Cys Ser Val Thr Val Val Phe Val
        1240                1245                1250

atg acg cag gga gac ccc gtg ttc gac gac aac gca gct tct gtc cgc     3968
Met Thr Gln Gly Asp Pro Val Phe Asp Asp Asn Ala Ala Ser Val Arg
    1255                1260                1265

ttc gtt gaa aag gaa gct ggt atg tcg gaa aag ttt cag ctg cct cag     4016
Phe Val Glu Lys Glu Ala Gly Met Ser Glu Lys Phe Gln Leu Pro Gln
1270                1275                1280                1285

gcc gat gac ccc aaa aac tac agg tgt atg gac gac tgc cat acc atc     4064
Ala Asp Asp Pro Lys Asn Tyr Arg Cys Met Asp Asp Cys His Thr Ile
                1290                1295                1300

tac tac tct atc gtt gat ggc aac gat ggt gac cac ttc gcc gtg gag     4112
Tyr Tyr Ser Ile Val Asp Gly Asn Asp Gly Asp His Phe Ala Val Glu
            1305                1310                1315

ccg gag act aac gtg atc tat ttg ctg aag ccg ctg gac cgc agc caa     4160
Pro Glu Thr Asn Val Ile Tyr Leu Leu Lys Pro Leu Asp Arg Ser Gln
        1320                1325                1330

cag gag cag tac agg gtc gtg gtg gcg gct tcc aac acg cct ggc ggc     4208
Gln Glu Gln Tyr Arg Val Val Val Ala Ala Ser Asn Thr Pro Gly Gly
    1335                1340                1345

acc tcc acc ttg tcc tcc tca ctc ctc acc gtc acc atc ggc gtt cga     4256
Thr Ser Thr Leu Ser Ser Ser Leu Leu Thr Val Thr Ile Gly Val Arg
1350                1355                1360                1365

gaa gca aac cct aga ccg atc ttc gaa agt gaa ttt tac aca gct ggc     4304
Glu Ala Asn Pro Arg Pro Ile Phe Glu Ser Glu Phe Tyr Thr Ala Gly
                1370                1375                1380

gtc tta cac acc gat agc ata cac aag gag ctc gtt tac ctg gcg gca     4352
Val Leu His Thr Asp Ser Ile His Lys Glu Leu Val Tyr Leu Ala Ala
            1385                1390                1395

aaa cat tca gaa ggg ctt cct atc gtc tac tcg ata gat caa gaa acc     4400
Lys His Ser Glu Gly Leu Pro Ile Val Tyr Ser Ile Asp Gln Glu Thr
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        1400                1405                1410

atg aaa ata gac gag tcg ttg caa aca gtt gtg gag gac gcc ttc gac      4448
Met Lys Ile Asp Glu Ser Leu Gln Thr Val Val Glu Asp Ala Phe Asp
    1415                1420                1425

att aac tct gca acc gga gtc ata tcg ctg aac ttc cag cca aca tct      4496
Ile Asn Ser Ala Thr Gly Val Ile Ser Leu Asn Phe Gln Pro Thr Ser
1430                1435                1440                1445

gtc atg cac ggc agt ttc gac ttc gag gtg gtg gct agt gac acg cgt      4544
Val Met His Gly Ser Phe Asp Phe Glu Val Val Ala Ser Asp Thr Arg
                1450                1455                1460

gga gcg agt gat cga gca aaa gtg tca att tac atg ata tcg act cgc      4592
Gly Ala Ser Asp Arg Ala Lys Val Ser Ile Tyr Met Ile Ser Thr Arg
            1465                1470                1475

gtt aga gta gcc ttc ctg ttc tac aac acg gaa gct gaa gtt aac gag      4640
Val Arg Val Ala Phe Leu Phe Tyr Asn Thr Glu Ala Glu Val Asn Glu
        1480                1485                1490

aga aga aat ttc att gca caa acg ttc gcc aac gcg ttt ggt atg aca      4688
Arg Arg Asn Phe Ile Ala Gln Thr Phe Ala Asn Ala Phe Gly Met Thr
    1495                1500                1505

tgt aac ata gac agc gtg ctg ccg gct acc gac gcc aac ggc gtg att      4736
Cys Asn Ile Asp Ser Val Leu Pro Ala Thr Asp Ala Asn Gly Val Ile
1510                1515                1520                1525

cgc gag ggg tac aca gaa ctc cag gct cac ttc ata cga gac gac cag      4784
Arg Glu Gly Tyr Thr Glu Leu Gln Ala His Phe Ile Arg Asp Asp Gln
                1530                1535                1540

ccg gtg cca gcc gac tat att gag gga tta ttt acg gaa ctc aat aca      4832
Pro Val Pro Ala Asp Tyr Ile Glu Gly Leu Phe Thr Glu Leu Asn Thr
            1545                1550                1555

ttg cgt gac atc aga gag gta ctg agt act cag caa ttg acg cta ctg      4880
Leu Arg Asp Ile Arg Glu Val Leu Ser Thr Gln Gln Leu Thr Leu Leu
        1560                1565                1570

gac ttt gcg gcg gga ggg tcg gca gtg ctg ccc ggc gga gag tac gcg      4928
Asp Phe Ala Ala Gly Gly Ser Ala Val Leu Pro Gly Gly Glu Tyr Ala
    1575                1580                1585

cta gcg gtg tac atc ctc gcc ggc atc gca gcg tta ctc gcc gtc atc      4976
Leu Ala Val Tyr Ile Leu Ala Gly Ile Ala Ala Leu Leu Ala Val Ile
1590                1595                1600                1605

tgt ctc gct ctc ctc atc gct ttc ttc att agg aac cga aca ctg aac      5024
Cys Leu Ala Leu Leu Ile Ala Phe Phe Ile Arg Asn Arg Thr Leu Asn
                1610                1615                1620

cgg cgc atc gaa gcc ctc aca atc aaa gat gtt cct acg gac atc gag      5072
Arg Arg Ile Glu Ala Leu Thr Ile Lys Asp Val Pro Thr Asp Ile Glu
            1625                1630                1635

cca aac cac gcg tca gta gca gtg cta aac att aac aag cac aca gaa      5120
Pro Asn His Ala Ser Val Ala Val Leu Asn Ile Asn Lys His Thr Glu
        1640                1645                1650
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cct ggt tcc aat ccc ttc tat aac ccg gat gtt aag aca cct aac ttc 5168
Pro Gly Ser Asn Pro Phe Tyr Asn Pro Asp Val Lys Thr Pro Asn Phe
1655 1660 1665

gac act ata agc gaa gta tcc gat gac ctg ctt gat gtc gaa gac ttg 5216
Asp Thr Ile Ser Glu Val Ser Asp Asp Leu Leu Asp Val Glu Asp Leu
1670 1675 1680 1685

gaa cag ttt gga aag gat tac ttc cca ccc gaa aac gaa att gag agc 5264
Glu Gln Phe Gly Lys Asp Tyr Phe Pro Pro Glu Asn Glu Ile Glu Ser
1690 1695 1700

ctg aat ttt gca cgt aac ccc ata gcg aca cac ggg aac aac ttt ggc 5312
Leu Asn Phe Ala Arg Asn Pro Ile Ala Thr His Gly Asn Asn Phe Gly
1705 1710 1715

gta aac tca agc ccc tcc aac cca gag ttc tcc aac tcc cag ttt aga 5360
Val Asn Ser Ser Pro Ser Asn Pro Glu Phe Ser Asn Ser Gln Phe Arg
1720 1725 1730

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Ser

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35 40 45
Trp Ala Gln Gln Pro Leu Leu Pro Ala Glu Asp Arg Glu Glu Val Cys
50 55 60
Leu Asn Asp Tyr Glu Pro Asp Pro Trp Ser Asn Asn His Gly Asp Gln
65 70 75 80
Arg Ile Tyr Met Glu Glu Glu Ile Glu Gly Pro Val Val Ile Ala Lys
85 90 95
Ile Asn Tyr Gln Gly Asn Thr Pro Pro Gln Ile Arg Leu Pro Phe Arg
100 105 110
Val Gly Ala Ala His Met Leu Gly Ala Glu Ile Arg Glu Tyr Pro Asp
115 120 125
Ala Thr Gly Asp Trp Tyr Leu Val Ile Thr Gln Arg Gln Asp Tyr Glu
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Thr Pro Asp Met Gln Arg Tyr Thr Phe Asp Val Ser Val Glu Gly Gln
145 150 155 160
Ser Leu Val Val Thr Val Arg Leu Asp Ile Val Asn Ile Asp Asp Asn
165 170 175
Ala Pro Ile Ile Glu Met Leu Glu Pro Cys Asn Leu Pro Glu Leu Val
180 185 190
Glu Pro His Val Thr Glu Cys Lys Tyr Ile Val Ser Asp Ala Asp Gly
195 200 205
Leu Ile Ser Thr Ser Val Met Ser Tyr His Ile Asp Ser Glu Arg Gly
210 215 220

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Asp Glu Lys Val Phe Glu Leu Ile Arg Lys Asp Tyr Pro Gly Asp Trp
225                 230                 235                 240
Thr Lys Val Tyr Met Val Leu Glu Leu Lys Lys Ser Leu Asp Tyr Glu
                245                 250                 255
Glu Asn Pro Leu His Ile Phe Arg Val Thr Ala Ser Asp Ser Leu Pro
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Asn Asn Arg Thr Val Val Met Met Val Glu Val Glu Asn Val Glu His
        275                 280                 285
Arg Asn Pro Arg Trp Met Glu Ile Phe Ala Val Gln Gln Phe Asp Glu
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Lys Gln Ala Lys Ser Phe Thr Val Arg Ala Ile Asp Gly Asp Thr Gly
305                 310                 315                 320
Ile Asn Lys Pro Ile Phe Tyr Arg Ile Glu Thr Glu Asp Glu Asp Lys
                325                 330                 335
Glu Phe Phe Ser Ile Glu Asn Ile Gly Glu Gly Arg Asp Gly Ala Arg
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Phe His Val Ala Pro Ile Asp Arg Asp Tyr Leu Lys Arg Asp Met Phe
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His Ile Arg Ile Ile Ala Tyr Lys Gln Gly Asp Asn Asp Lys Glu Gly
    370                 375                 380
Glu Ser Ser Phe Glu Thr Ser Ala Asn Val Thr Ile Ile Ile Asn Asp
385                 390                 395                 400
Ile Asn Asp Gln Arg Pro Glu Pro Phe His Lys Glu Tyr Thr Ile Ser
                405                 410                 415
Ile Met Glu Glu Thr Ala Met Thr Leu Asp Leu Gln Glu Phe Gly Phe
            420                 425                 430
His Asp Arg Asp Ile Gly Pro His Ala Gln Tyr Asp Val His Leu Glu
        435                 440                 445
Ser Ile Gln Pro Glu Gly Ala His Thr Ala Phe Tyr Ile Ala Pro Glu
    450                 455                 460
Glu Gly Tyr Gln Ala Gln Ser Phe Thr Ile Gly Thr Arg Ile His Asn
465                 470                 475                 480
Met Leu Asp Tyr Glu Asp Asp Asp Tyr Arg Pro Gly Ile Lys Leu Lys
                485                 490                 495
Ala Val Ala Ile Asp Arg His Asp Asn Asn His Ile Gly Glu Ala Ile
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Ile Asn Ile Asn Leu Ile Asn Trp Asn Asp Glu Leu Pro Ile Phe Asp
        515                 520                 525
Glu Asp Ala Tyr Asn Val Thr Phe Glu Glu Thr Val Gly Asp Gly Phe
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His Ile Gly Lys Tyr Arg Ala Lys Asp Arg Asp Ile Gly Asp Ile Val
545                 550                 555                 560
Glu His Ser Ile Leu Gly Asn Ala Ala Asn Phe Leu Arg Ile Asp Ile
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Asp Thr Gly Asp Val Tyr Val Ser Arg Asp Asp Tyr Phe Asp Tyr Gln
            580                 585                 590
Arg Gln Asn Glu Ile Ile Val Gln Ile Leu Ala Val Asp Thr Leu Gly
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    610                 615                 620
Ile Asn Asn Thr Pro Pro Ile Leu Arg Leu Pro Arg Ser Ser Pro Ser
625                 630                 635                 640
Val Glu Glu Asn Val Glu Val Gly His Pro Ile Thr Glu Gly Leu Thr
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Ala Thr Asp Pro Asp Thr Thr Ala Asp Leu His Phe Glu Ile Asp Trp
            660                 665                 670
Asp Asn Ser Tyr Ala Thr Lys Gln Gly Thr Asn Gly Pro Asn Thr Ala
        675                 680                 685
Asp Tyr His Gly Cys Val Glu Ile Leu Thr Val Tyr Pro Asp Pro Asp
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Asn His Gly Arg Ala Glu Gly His Leu Val Ala Arg Glu Val Ser Asp
705                 710                 715                 720
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Gly Val Thr Ile Asp Tyr Glu Lys Phe Glu Val Leu Tyr Leu Val Val
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Arg Val Ile Asp Arg Asn Thr Val Ile Gly Pro Asp Tyr Asp Glu Ala
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Met Leu Thr Val Thr Ile Ile Asp Met Asn Asp Asn Trp Pro Ile Trp
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Ala Asp Asn Thr Leu Gln Gln Thr Leu Arg Val Arg Glu Met Ala Asp
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Glu Gly Val Ile Val Gly Thr Leu Leu Ala Thr Asp Leu Asp Gly Pro
785                 790                 795                 800
Leu Tyr Asn Arg Val Arg Tyr Thr Met Val Pro Ile Lys Asp Thr Pro
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Asp Asp Leu Ile Ala Ile Asn Tyr Val Thr Gly Gln Leu Thr Val Asn
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Lys Gly Gln Ala Ile Asp Ala Asp Asp Pro Pro Arg Phe Tyr Leu Tyr
        835                 840                 845
Tyr Lys Val Thr Ala Ser Asp Lys Cys Ser Leu Asp Glu Phe Phe Pro
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Val Cys Pro Pro Asp Pro Thr Tyr Trp Asn Thr Glu Gly Glu Ile Ala
865                 870                 875                 880
Ile Ala Ile Thr Asp Thr Asn Asn Lys Ile Pro Arg Ala Glu Thr Asp
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Met Phe Pro Ser Glu Lys Arg Ile Tyr Glu Asn Thr Pro Asn Gly Thr
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Lys Ile Thr Thr Ile Ile Ala Ser Asp Gln Asp Arg Asp Arg Pro Asn
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Asn Phe Phe Ala Val Asp Pro Asp Thr Gly Glu Leu Phe Val His Phe
945                 950                 955                 960
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(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
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(10) International Publication Number
WO 01/36639 A3

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(21) International Application Number: PCT/US00/31674

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60/234,099 21 September 2000 (21.09.2000) US

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(74) Agents: SPRUILL, Murray, W. et al.; Alston & Bird LLP, Bank of America Plaza, 101 South Tryon Street, Suite 4000, Charlotte, NC 28280-4000 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AT (utility model), AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, CZ (utility model), DE, DE (utility model), DK, DK (utility model), DM, DZ, EE, EE (utility model), ES, FI, FI (utility model), GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK (utility model), SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

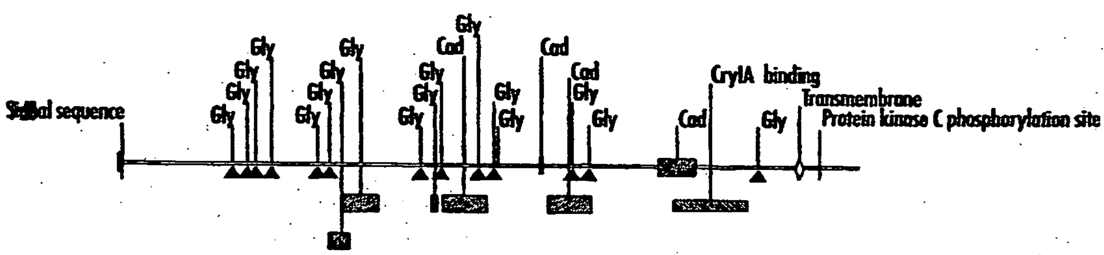
(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

(88) Date of publication of the international search report:
22 November 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: BT TOXIN RECEPTORS FROM LEPIDOPTERAN INSECTS AND METHODS OF USE



OnBIR1 (E19C2)
1717 aa

Gly = putative glycosilation sites

Cad = cadherin-like domain

(57) Abstract: The invention relates to *Bt* toxin resistance management. The invention particularly relates to the isolation and characterization of nucleic acid and polypeptides for a novel *Bt* toxin receptor. The nucleic acid and polypeptides are useful in identifying and designing novel *Bt* toxin receptor ligands including novel insecticidal toxins.

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INTERNATIONAL SEARCH REPORT

Intern. ...al Application No
PCT/US 00/31674

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C12N15/62 C12N5/10 C07K14/705 C07K16/28 G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

WPI Data, PAJ, CAB Data, STRAND, BIOSIS, EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	NAGAMATSU YASUNORI ET AL: "Cloning, sequencing, and expression of the Bombyx mori receptor for Bacillus thuringiensis insecticidal CryIA(a) toxin." BIOSCIENCE BIOTECHNOLOGY AND BIOCHEMISTRY, vol. 62, no. 4, April 1998 (1998-04), pages 727-734, XP002164759 ISSN: 0916-8451 cited in the application the whole document	1,2,4, 9-15
X	WO 96 12964 A (UNIV WYOMING) 2 May 1996 (1996-05-02) the whole document	1,2,4, 9-15, 19-22

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
13 June 2001	29.06.01

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31–70) 340–2040, Tx. 31 651 epo nl, Fax: (+31–70) 340–3016	Hornig, H

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	VADLAMUDI RATNA K ET AL: "Cloning and expression of a receptor for an insecticidal toxin of Bacillus thuringiensis." JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 10, 1995, pages 5490-5494, XP002164760 ISSN: 0021-9258 cited in the application the whole document	1,2,4, 9-15
X	KEETON TIMOTHY P ET AL: "Ligand specificity and affinity of BT-R-1, the Bacillus thuringiensis Cry1A toxin receptor from Manduca sexta, expressed in mammalian and insect cell cultures." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 63, no. 9, 1997, pages 3419-3425, XP002164761 ISSN: 0099-2240 cited in the application the whole document	1,2,4, 9-15
X	KEETON TIMOTHY P ET AL: "Effects of midgut-protein-preparative and ligand binding procedures on the toxin binding characteristics of BT-R1, a common high-affinity receptor in Manduca sexta for Cry1A Bacillus thuringiensis toxins." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 64, no. 6, June 1998 (1998-06), pages 2158-2165, XP002164762 ISSN: 0099-2240 cited in the application the whole document	1,2,4, 9-15
A	GILL SARJEET S ET AL: "Identification, isolation, and cloning of a Bacillus thuringiensis CryIAc toxin-binding protein from the midgut of the lepidopteran insect Heliothis virescens." JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 45, 1995, pages 27277-27282, XP002164763 ISSN: 0021-9258 cited in the application the whole document	

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INTERNATIONAL SEARCH REPORT

Intern   nal Application No
PCT/US 00/31674

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	LEE MI KYONG ET AL: "Aminopeptidase N purified from gypsy moth brush border membrane vesicles is a specific receptor for Bacillus thuringiensis CryIAc toxin." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 62, no. 8, 1996, pages 2845-2849, XP002164764 ISSN: 0099-2240 cited in the application the whole document	
E	WO 01 34807 A (CANDAS MEHMET ;BULLA LEE A JR (US)) 17 May 2001 (2001-05-17) claims 1-28; figures 1,2	1-15
A	GARCZYNSKI S F ET AL: "IDENTIFICATION OF PUTATIVE INSECT BRUSH BORDER MEMBRANE-BINDING MOLECULES SPECIFIC TO BACILLUS-THURINGIENSIS DELTA ENDOTOXIN BY PROTEIN BLOT ANALYSIS" APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 57, no. 10, 1991, pages 2816-2820, XP000992668 ISSN: 0099-2240 the whole document	
A	OLTEAN DANIELA I ET AL: "Partial purification and characterization of Bacillus thuringiensis Cry1A toxin receptor A from Heliothis virescens and cloning of the corresponding cDNA." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 65, no. 11, November 1999 (1999-11), pages 4760-4766, XP002169506 ISSN: 0099-2240 the whole document	

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International application No.
PCT/US 00/31674

INTERNATIONAL SEARCH REPORT

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: (1-25)-partially

   An isolated nucleic acid molecule having the nucleotide sequence encoding a Bt toxin receptor, selected from Ostrinia nubilalis respectively SEQ ID No. 1; said nucleic acid, wherein said toxin is Cry1A/Cry1A(b); an isolated polypeptide having the amino acid sequence set forth in SEQ ID NO. 2; a fusion polypeptide comprising said polypeptide, an expression cassette comprising a nucleotide sequence encoding said fusion polypeptide; an antibody preparation specific for said polypeptide; a vector comprising said expression cassette; a cell comprising said vector; a transformed cell of interest having stably incorporated within its genome said nucleotide sequence, SEQ ID No.1; a method for screening for ligands that bind said Bt toxin receptor comprising SEQ ID No. 2;

2. Claims: (1-25)-partially

   Idem as invention 1 but limited to Heliothis zea, respectively SEQ ID Nos. 3 and 4;

3. Claims: (1-25)-partially

   Idem as invention 1 but limited to Spodoptera frugiperda, respectively SEQ ID Nos. 5 and 6;

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/US 00/31674

Patent document cited in search report		Publication date	Patent family member(s)			Publication date
WO 9612964	A	02-05-1996	US	5693491	A	02-12-1997
			AU	711066	B	07-10-1999
			AU	4001595	A	15-05-1996
			CA	2200427	A	02-05-1996
			EP	0787299	A	06-08-1997
			JP	10508198	T	18-08-1998
			NZ	296265	A	28-05-1999
			US	6007981	A	28-12-1999
			ZA	9508851	A	11-06-1996
WO 0134807	A	17-05-2001	NONE			